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DEFINITION Sequence 2 from Patent WO9958690.
ACCESSION AX010482
VERSION AX010482.1 GI:9997326
KEYWORDS
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ORGANISM
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Poaceae; Triticeae; Triticum.
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REFERENCE
1. Lueticke, S., Abel, G., Loez, H. and Genschel, U.
Nucleic acid molecules which code for enzymes derived from wheat
and which are involved in the synthesis of starch
Patent: WO 9958690-A 2 18-NOV-1999.
LUTETICKE STRAPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);
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VERSION AJ307689.1 GI:14331017
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REFERENCE
1 Genschel,U., Gernot,A., Lorz,H. and Luetticke,S.
The sugary-type isoamylase in wheat: tissue distribution and
subcellular localisation
Online Publication
Planta, DOI 10.1007/s00425-001-0691-3
REFERENCE
2 Genschel,U., Abel,G., Lorz,H. and Luetticke,S.
The sugary-type isoamylase in wheat
Unpublished
3 (bases 1 to 2997)
AUTHORS Luetticke,S.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2001) Luetticke S., Insitut fuer Allgemeine
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Db 1604 ----- 1603  
Qy 2101 CAGTAACTTGTATTGGCCTGCACTGCAACTTCTTATTGATTATCAGGAGGAGGAGGAAC 2160  
Db 1604 ----- 1622  
Qy 2161 CTTGGCAGATCAACTTTGTATGTGCATATGATGATTTACACTGGCTGATTTGGTAA 2220  
Db 1623 CTTGGCAGATCAACTTTGTATGTGCATATGATGATTTACACTGGCTGATTTGGTAA 1682  
Qy 2221 CATATAATAAGATGATAAATTTACAAATGGGGAGAACACAGAGATGGAGAAATCACA 2280  
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Db 2403 GTAAATATATGCTATATGTA 2424

RESULT 5  
AF548380  
LOCUS

AF548380 2574 bp mRNA linear PLN 29-MAY-2003

DEFINITION	Triticum aestivum isoamylase wDBE-D1 mRNA, complete cds.	
ACCESSION	AF548380	
VERSION	AF548380.1	GI:31096627
KEYWORDS		
SOURCE	Triticum aestivum (bread wheat)	
ORGANISM	Triticum aestivum	
REFERENCE	Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.	
AUTHORS	Rahman, S., Nakamura, Y., Li, Z., Clarke, B., Fujita, N., Mukai, Y., Yamamoto, M., Regina, A., Tan, Z., Kawasaki, S. and Morell, M.	
TITLE	The sugary-type isoamylase gene from rice and Aegilops tauschii: characterization and comparison with maize and Arabidopsis	
JOURNAL	Genome 46 (3), 496-506 (2003)	
REFERENCE	2 (bases 1 to 2574)	
AUTHORS	Rahman, S., Li, Z., Clarke, B., Regina, A. and Morell, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-SEP-2002) Plant Industry, CSIRO, Clunies Ross, Canberra, ACT 2615, Australia	
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ORIGIN		
Query Match	54.0%; Score 1617.4; DB 8; Length 2574;	
Best Local Similarity	77.5%; Pred. No. 7.6e-307;	
Matches 2299; Conservative	0; Mismatches 36; Indels 530; Gaps 3;	
Qy	1	GGTGGGGCGGGCGCGCGCTGCGACGGTGGGACCCCAATGCGCGGGGAAAGGGG 60
Db	178	GGCGGGCGGGCGCGCGCTGCGACGGTGGGACCCCAATGCGCGGGGAAAGGGG 237
Qy	61	TCGCGGAGGTGTGCGCGCGGTGTGCGAGCGGCGAGAGGTAGAGGACGAG- --GGG 117
Db	238	TCGCGGAGGTGTGCGCGCGGTGTGCGAGCGGCGAGAGGCGGAGGAGGACGACG 297
Qy	118	AGGAGGACGAGCGCGGTGGCGAGGACAGGTACGCGCTCGCGCGGCGGTGCGAGGTGCTG 177
Db	298	ACGAGGAGGAGCGGTGGCGAGGACAGGTACGCGCTCGCGCGGCGGTGCGAGGTGCTG 357
Qy	178	CCGGAATGCCCGCGCGCTGGCGCCACCGCGCTCGCGCGGCGGTCAATTCGCGCTCT 237
Db	358	CCGGAATGCCCGCGCGCTGGCGCCACCGCGCTCGCGCGGCGGTCAATTCGCGCTCT 417
Qy	238	ATTCGCGGAGGACCGCGCGCGCGCTCTGCGCTCTTCACGCCAGAGATCTCAAGCGG 297
Db	418	ACTCCGCTGGAGCCACCGCGCGCGCTCTGCGCTCTTCACGCCAGAGATCTCAAGC- - 475

Qy	298	TGGGTTGCTCCTCCGAGTAGAGTTTCATCAGCTTTTCGTCGCGCGCGCGCTTTTGG 357
Db	476	-----
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Db	476	-----GGATAGGCTGACCGAGAGGTT 497
Qy	418	CCCCCTGACCCCTGATGAATCGGACCGGAAACGTGTGGCATGTCTTCATCGAAGCGAG 477
Db	498	TCCTTTGACCCCTGATGAATCGGACCGGAAACGTGTGGCATGTCTTCATTTGAAGCGAG 557
Qy	478	CTGCAACAATGCTTTTACGGGTACAGGTTCGACGGCACCTTTGCTCTCATCTCGGGCAC 537
Db	558	CTGCAACAATGCTTTTACGGGTACAGGTTCGACGGCACCTTTGCTCTCATCTCGGGCAC 617
Qy	538	TACCTTGATGTTTCCAAATGCTGTGTGATCCTTATGCTTAAGGACGATGAAGCCGAGG 597
Db	618	TACCTTGATGTTTCCAAATGCTGTGTGATCCTTATGCTTAAGGACGATGAAGCCGAGG 677
Qy	598	GAGTATGCTGTTCCAGCGCGTGTAAACAATTCCTGGCTCAGATGGCTGGCATGATCCT 657
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Qy	658	CTTCCATATAGCAGCTTTGATGCGAAGCGACCTACCTCTAAGATCTCTCAAGAGGAC 717
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Qy	718	CTGTTAATATATAGATGACATCCTTGGTGGATTACGAAGACGATGATTCAAGCAATAGAA 777
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Qy	778	CATCGGGTACTTTCAATGGAGCTGTGCGAAGCTTGATATTTGAAGAGCTTGGAGTT 837
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Qy	838	AATTGTTGAATTAATCCCTGCCATCAGTTCAACGAGCTGGAGTACTCAACCTCTCT 897
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Qy	898	TCCAAGATGAATTTTGGGATATTCTACCAATAAATCTTTTCCCAATGACAGATAC 957
Db	978	TCCAAGATGAATTTTGGGATATTCTACCAATAAATCTTTTCCCAATGACAGATAC 1037
Qy	958	ACATCAGCGGGATAAAAAATGTTGGGCGTGCATGCCATAAATGAGTTCAAACTTTGTA 1017
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Qy	1018	AGAGAGGCTCAAAAACGGGGAATTCAGGTGATCCTGGATGTTGCTTCAACCATACAGCT 1077
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Qy	1078	GAGGTATAGAGATGTTCCAAATATTATTAAGGGGTCGATAATACTACATACTAT 1137
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Qy	1138	ATGCTTGACCAACGAGGAGGTTTTATAACTATTCTGCTGCGGAATACCTTCAACTGT 1197
Db	1218	ATGCTTGACCAACGAGGAGGTTTTATAACTATTCTGCTGCGGAATACCTTCAACTGT 1277
Qy	1198	AATCATCTGCTGTTTCGCAATTCATGTAAGTTTAAAGATACTGGGTGACGGAATG 1257
Db	1278	AATCATCTGCTGTTTCGCAATTCATGTAAGTTTAAAGATACTGGGTGACGGAATG 1337
Qy	1258	CATGTTGATGTTTTCGTTTTCATCTTCATCCATAATGACGAGGTTCCAGTCTGTTG 1317
Db	1338	CATGTTGATGTTTTCGTTTTCATCTTCATCCATAATGACGAGGTTCCAGTCTGTTG 1397
Qy	1318	GATCCAGTTAAGCTGATGGAGCTCCAAATAGAAGTGCATGATCACAACAGGACACT 1377
Db	1398	GATCCAGTTAAGCTGATGGAGCTCCAAATAGAAGTGCATGATCACAACAGGACACT 1457
Qy	1378	CTTGTACTCCACCACTTATTGACATGATGACCAATGATGCCAATTTCTTGGAGGCTCAG 1437

[illegible]

Db	2011	ATGATCTTTATGTCAAATATTATTTTCGTGGGATAAAAAGAACAAATACTCTGACTTGCACA	2077
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Db	2071	GATTCTGCTGCCTCATGACCAAAATTCGCAAGAGTGCAGAGGTCTTTGGCCCTTGAGGACT	2130
Qy	2578	TTCCACAGCGCCAAACGGCTGCAGTGGCATGGTTCATCAGCCTGGGAAGCCTGATGGTCTG	2637
Db	2131	TTCCACAGCGCGCAACGGCTGCAGTGGCATGGTTCATCAGCCTGGGAAGCCTGATGGTCTG	2190
Qy	2638	AGAATACCGGATTCGTTTCCTTTTCCATGAAGATGAAGACAGAGCGAGATCTATGTGG	2697
Db	2191	AGAATACCGGATTCGTTTCCTTTTCCATGAAGATGAAGACAGAGCGAGATCTATGTGG	2250
Qy	2698	CCTTCAACACCGCCACTTACCGGCGCTTGTTCAGTCTCCAGAGCGCGAGGCGCGCGGT	2757
Db	2251	CCTTCAACACCGCCACTTACCGGCGCTTGTTCAGTCTCCAGAGCGCGAGGCGCGCGGT	2310
Qy	2758	GGGAACCGGTGGTGGACACAGCAAGCCAGCACCATACGACTTCTTCCACCGAGCATTTAC	2817
Db	2311	GGGAACCGGTGGTGGACACAGCAAGCCAGCACCATACGACTTCTTCCACCGAGCATTTAC	2370
Qy	2818	CTGATCGCGCTCTCACCATAACACAGTTCTCGCATTCCTCTACTCTCAACCTCTACCCCA	2877
Db	2371	CTGATCGCGCTCTCACCATAACACAGTTCTCTCATTTCTCAACCTCTACCCCA	2430
Qy	2878	TGCTCAGCTACTCATCGGTTCATCCTAGTATTCGGCCCTCATGTTTCAGAGACCAATATAT	2937
Db	2431	TGCTCAGCTACTCATCGGTTCATCCTAGTATTCGGCCCTCATGTTTCAGAGACCAATATAT	2490
Qy	2938	ACAGTAATAATATGCTATATGTA	2962
Db	2491	ACAGTAATAATATGCTATATGTA	2515
RESULT 6			
LOCUS	TAE301647	2490 bp	linear
DEFINITION	Triticum aestivum mRNA for isoamylase (isol gene).		
ACCESSION	AJ301647		
VERSION	AJ301647.1	GI:17932897	
KEYWORDS	isol gene; isoamylase.		
SOURCE	Triticum aestivum (bread wheat)		
ORGANISM	Triticum aestivum		
REFERENCE	1 Genschel, U., Gernot, A., Lorz, H. and Luetticke, S.		
AUTHORS	The sugary-type isomylase in wheat: tissue distribution and		
TITLE	subcellular localisation		
JOURNAL	Online Publication		
REMARK	Planca, DOI 10.1007/s00425-001-0691-3		
REFERENCE	2 (bases 1 to 2490)		
AUTHORS	Genschel, U.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-NOV-2000) Genschel U., Institut fuer Allgemeine		
REMARK	Botanik, AMP II, Universitaet Hamburg, Ohnhorststrasse 18, Hamburg,		
COMMENT	22609, Germany		
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Qy	721	GTAATATAG	ATGAGTGCAC	TCCTGGTATTCGAAAGCATGATTCAGCAATGTAGAACAT	780
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Qy	781	CCGGTACT	TTTCATTTGGAGCT	GTGTCGAGCTTCGACTATTTGAAGAGCTTGGAGTTAAT	840
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Qy	841	TGTATTGA	TTAAATGCCCTG	CCATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCC	900
Db	807	TGTATTGA	TTAAATGCCCTG	CCATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCC	866
Qy	901	AAGATGAA	CTTTTGGGGATAT	CTACATAAATCTTTTCCACCATGACAGATACACA	960
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Qy	961	TCAGGCGG	ATAAAAACTGT	GGGCGTCATGCCATAATGAGTTCAAACTTTTGTAAAG	1020
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Qy	1021	GAGGCTCA	CAAAACGGGAA	TTGAGGTGATCTCTGAGTGTCTTCCAAACATACAGCTGAG	1080
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Qy	1081	GATATGAA	TGTCCTCAAT	TATCAATTAAGGGGTCGATATACATACATATATATG	1140
Db	1047	GATATGAA	TGTCCTCAAT	TATCAATTAAGGGGTCGATATACATACATATATATG	1106
Qy	1141	CTTGACCA	CCAAAGGAGAG	TTTTTATAACTATTCTGGCTGGGAATACCTTCAACTGTAA	1200
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Qy	121	AGGACGAG	CGCGGAGG	ACAGGTACGCGCTCGCGCGGCTGCGAGGCTCTCGCGG	180
Db	187	AGGACGAG	CGCGGAGG	ACAGGTACGCGCTCGCGCGGCTGCGAGGCTCTCGCGG	246
Qy	181	GAATGCGG	CGCGCGCTG	CGCGCGGACCGCTCGCGCGGCGGCTCAATTCGCGCTCTATT	240
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Qy	301	GGTTGCTC	CGGAGTAGAG	TTTCAATGAGTTTGGCTGCGCGCGGCGGCTTTTGGGCGC	360
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Qy	361	TGCAATTA	AGTTTGTACT	GGGCAAAATGCTGCAGGATAGGTTGACGAGGAGTTTCCC	420
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Qy	421	CTTGACCC	CGCTGATGA	TTCGACCGGAACTGTGCGATGTCTTCATCGAAGCGAGCTG	480
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Qy	481	CACACATG	CTTTACGGG	TACAGGTTGACGCGGACCTTTGCTCTCACTGGGCGACTAC	540
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Qy	541	CTTCATGT	TTTCCAAATG	CTGCTGGATCTTATCTAAGGCGAGTGAAGCCGAGGGGAG	600
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Query Match 53.9%; Score 1614.8; DB 8; Length 2490;  
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Matches 2296; Conservative 0; Mismatches 37; Indels 629; Gaps 3;



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 AX010486  
 LOCUS  
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 SOURCE  
 ORGANISM  
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 Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Triticeae; Triticum.  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 LUSTTICKE, S., Abel, G., Loerz, H. and Genschel, U.  
 Nucleic acid molecules which code for enzymes derived from wheat  
 and which are involved in the synthesis of starch  
 Patent: WO 958690-A 6 18-NOV-1999;  
 LUSTTICKE STRAPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);  
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source  
 CDS  
 ORIGIN  
 Query Match 53.8%; Score 1611.8; DB 6; Length 2437;  
 Best Local Similarity 77.5%; Pred. No. 9.4e-306;  
 Matches 2293; Conservative 0; Mismatches 37; Indels 629; Gaps 3;  
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 Db 71 CGAGGCTGTGCGCGCGCGCTGTGAGGTCGCGAGGAGGAGGAGGAGGAGG 130

QY 124 ACAGCCGCTGGCGGAGCAGGTACGGCTCGCGCGCGTGCAGGGTCTCGCCGGA 193  
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Db	2322	AATATATGCTATATGTA	2340
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DEFINITION	Hordeum vulgare isoamylase mRNA, complete cds.		
ACCESSION	AF490375		
VERSION	AF490375.1 GI:21314274		
KEYWORDS			
SOURCE	Hordeum vulgare subsp. vulgare		
ORGANISM	Hordeum vulgare subsp. vulgare		
REFERENCE	1 (bases 1 to 2495)		
AUTHORS	Burton, R.A., Jenner, H., Carrangis, L., Fahy, B., Fincher, G.B., Hyllton, C., Laurie, D.A., Parker, M., Waite, D., van Wegen, S., Verhoeven, T. and Denyer, K.		
TITLE	Starch granule initiation and growth are altered in barley mutants that lack isoamylase activity		
JOURNAL	Plant J. 31 (1), 97-112 (2002)		
MEDLINE	22096154		
PUBMED	12100486		
REFERENCE	2 (bases 1 to 2495)		
AUTHORS	Burton, R.A., Denyer, K. and Fincher, G.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-MAR-2002) Plant Science, University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia		

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RESULT 9  
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LOCUS Hordeum vulgare hviisol gene for isoamylase, complete cds.  
DEFINITION AB074189  
ACCESSION AB074189  
VERSION 1  
KEYWORDS AB074189.1 GI:16923278  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Hordeum.  
1  
Komatsu, A., Kato, T. and Komae, K.  
Isolation of isoamylase gene in barley  
Published Only in Database (2001)  
2 (bases 1 to 2584)  
Komatsu, A. and Komae, K.  
Direct Submission  
Submitted (12-NOV-2001) Akira Komatsu, National Institute of Crop  
Science, Laboratory of Wheat and Barley Quality; 2-1-18 Kannondai,  
Tsukuba, Ibaraki 305-8518, Japan (E-mail: akomatsu@naro.affrc.go.jp,  
URL: http://nics.naro.affrc.go.jp/, Tel: 81-298-38-8945,  
Fax: 81-298-38-8949)  
Location/Qualifiers  
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ORIGIN

Query Match 50.4%; Score 1510.8; DB 8; Length 2584;  
Best Local Similarity 75.6%; Pred. No. 6.4e-286;  
Matches 2238; Conservative 0; Mismatches 92; Indels 632; Gaps 4;

QY 1 GGTGGGGCCGCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG 60  
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QY 61 TCGCGAGGTGTGCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG --G 117  
Db 233 TCGCGAGGTGTGCGCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG 292  
QY 118 AGGAGGACGCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG 177  
Db 293 AGGAGGAGCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG 352  
QY 178 CCGGAATGCCCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG 237  
Db 353 CCGGAATGCCCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGCGGGAAGGGG 412  
QY 238 ATTCCGGCGAGCGACCGCGCGCTGCGAGCGTGGCGACCAATGCGACGCGGGAAGGGG 297  
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QY 838 AATTGTATTGAATTAATGCCCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTTCT 897  
Db 913 AATTGTATTGAATTAATGCCCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTTCT 972  
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Db 973 TCCAGATGAACCTTTTGGGGATATTTTACCAATAAATCTTTTCCCAATGACAAGATAC 1032



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.

1 (bases 1 to 2445)  
Burton, R.A., Jenner, H., Carrangis, L., Fahy, B., Fincher, G.B., Hyton, C., Laurie, D.A., Parker, M., Waite, D., van Wegen, S., Verhoeven, T. and Denyer, K.

TITLE  
Starch granule initiation and growth are altered in barley mutants that lack isoamylase activity

JOURNAL  
Plant J. 31 (1), 97-112 (2002)

MEDLINE  
22096154

PUBMED  
12100486

REFERENCE  
2 (bases 1 to 2445)  
Burton, R.A., Denyer, K. and Fincher, G.B.

AUTHORS  
Direct Submission

TITLE  
Submitted (06-MAR-2002) Plant Science, University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia

JOURNAL  
Location/Qualifiers

FEATURES  
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ORIGIN  
Query Match 47.2%; Score 1414.2; DB 8; Length 2445;  
Best Local Similarity 73.7%; Pred. No. 5,7e-267;  
Matches 2209; Conservative 0; Mismatches 88; Indels 702; Gaps 4;

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Db 74 GGGCGGGGCGGGCGCGCGCTGCGAGGTGGCGACCCCAATGGCGCGGGGAAGGGG 133

Qy 61 TCGGCGAGGTGTGCGCGCGCGGTGTGCGAGGCGCGCGAGAGGTAGAGACGAGGGG ---G 117  
Db 134 TCGGCGAGGTGTGCGCGCGCGGTGTGCGAGGCGCGCGAGGCGCGAGGAGGAGACG 193

Qy 118 AGGAGGACGAGCGCGGTGGCGGAGACAGGTACGCGCTCGCGGCGCGCGGTGCGAGGTCGTCG 177  
Db 194 AGGAGGAGGAGCGCGGTGGCGGAGGAGGTATGCGCTCGGAGGCGCGGTGCGAGGTCGTCG 253

Qy 178 CCGGAATGCCCGT 237  
Db 254 CCGGAATGCCCGT 313

Qy 238 ATTCCGCGGAGCGACCGCGCGCGCGCTCTGCGCTCTTTCAACGCGAGAGATCTCAAGCGG 297  
Db 314 ACTCAGCGGAGCGACCGCGCGCGCGCTCTGCGCTCTTTCAACGCGAGAGATCTCAAGCG -- 371

Qy 298 TGGGGTTCGCTCCCGAGTAGATTTCATCAGCTTTGCGTGGCGCGCGCGCGCGCGCTTTTGG 357  
Db 372 ----- 371

358 GCCTCAATTTAAGTTTGTGTACTGGGGCAATGCTGCGAGGATAGGGTGACCGAGAGGTT 417  
Db 372 -----GGATAGGGTGAGCGAGAGGTT 393

Qy 418 CCCTTGAGCCCTTGATGAATCGGACCGGAACTGTGTGGGATGCTTCATCGAAGGGGAG 477  
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Db 874 TCCAGATGAATTTTGGGATATTTACCAATAACTCTTTTCCACCAATGACAGATAC 933

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Qy 1198 ATCATCTGTGGTTCGTCATTTGATGATGTTTAAAGTACTGGTTCACCGGAATG 1257  
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Qy 1258 CATGTTGATGTTTTCGTTTGTGATCTTGCATCCATAATGACAGAGGTTCC --- 1308  
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Qy 1309 ----- 1308

Db 1294 GCATTTATTATTGTTGTGTGCTTTTTCAGAGATTTCTTAGAATAATGTTTCTTTT 1353

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Db 1354 ACAAGTCTGTGGATCCCAATTAACGTGTATGAGGCTCCAATAGAGGTGACATGATCACA 1413

Qy 1366 ACAGGAGCACCTCTTGTGTACTCCACCACCTTATTGACATGATGACCAATGACCAATCTTT 1425





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## ORIGIN

Query Match 39.1%; Score 1171.6; DB 8; Length 1708;  
 Best Local Similarity 96.5%; Pred. No. 2.2e-219;  
 Matches 1198; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db	198	GCATGCTTTCATCGAAGCGGAGCTGCACGCGCATGCTTTATGGGTACAGGTTCCAGCGCAC	257
Qy	516	CTTTGCTCCTCACTGCGGCGCACTACCTTGTATGTTTCCAAATGTCGTGCTGATCCTTATGC	575
Db	258	CTTGCCTCCTCACTGCGGCGCACTACTTTGATGTTTCCAAATGTTGTTGCTGATCCTTATGC	317
Qy	576	TAAAGCATGATAGCGAGGAGGTATGTTTCCAGCGCTGTTAAACAAATTCCTGGCC	635
Db	318	TAAAGCATGATAGCGAGGAGGTATGTTTCCAGCGCTGTTAAACAAATTCCTGGCC	377
Qy	636	TCAGATGCTGCGCATGATCCTCTTCCATATAGCAGCTTTGATTGGGAGCGCACTACC	695
Db	378	TCAGATGCTGCGCATGATCCTCTTCCATATAGCAGCTTTGATTGGGAGCGCACTACC	437
Qy	696	TCTAAGATATCCTCAAAGGACCTGTGTAATATATGATGATGCACTTCGCTGGATTCACGAA	755
Db	438	TCTAAGATATCCTCAAAGGACCTGTGTAATATATGATGATGCACTTCGCTGGATTCACGAA	497
Qy	756	GCATGATCAAGCAATGATAGACATCCGGTACTTTTCATTTGGAGCTGTGCGAAGCTTGA	815
Db	498	GCATGATCAAGCAATGATAGACATCCGGTACTTTTCATTTGGAGCTGTGCGAAGCTTGA	557
Qy	816	CTATTTCAGAGAGCTTGGAGTTAATGTTTGAATTAATGCTGCTGATGATTCACGAA	875
Db	558	CTATTTCAGAGAGCTTGGAGTTAATGTTTGAATTAATGCTGCTGATGATTCACGAA	617
Qy	876	GCTGGAGTACTCAACTCTTCTTCCAGATGAATTTTGGGATATTTACCATTAACCTT	935
Db	618	GCTGGAGTACTCAACTCTTCTTCCAGATGAATTTTGGGATATTTACCATTAACCTT	677
Qy	936	CTTTTCCCAATGACAGATACACATCAGCGGGATATAAACTGTGGCGTGCATGCCAT	995
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Qy	996	AAATGAGTTCAAAACCTTTTGTAGAGAGGCTCAAAAACGGGGAATGAGGTATCTCTGGA	1055
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Qy	1056	TGTTGCTTCAACCATACAGCTGAGGTAATGAGATGCTCCATATATATCATTTAAGG	1115
Db	798	TGTTGCTTCAACCATACAGCTGAGGTAATGAGATGCTCCATATATATCATTTAAGG	857
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Db	858	GGTTGATAAATACATACATATATGCTTGCACCAACCGGAGAGTTTTATACATATTCCTGG	917
Qy	1176	CTGTGGGATACCTTCAACTGATATCATCTGTGGTTCGTCATTTCAATTCATTTAGATTTT	1235
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Qy	1236	AAGATACCTGGGTGACGGAATGCAATGTTGATGTTTTTCGTTTTGATCTTCCATCCATAAT	1295
Db	978	AAGATACCTGGGTGACGGAATGCAATGTTGATGTTTTTCGTTTTGATCTTCCATCCATAAT	1037
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Db	1038	GACCAGAGTTCACAGTCTGTGGGATCCAAATTAACGTGTATGGAGCTCCAATAGAGGTGA	1097
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Db	1098	CATGATCAACACAGGACACCTCTTGTACTCCACCCTATTATTCACATGATCAGCAATGA	1157
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Qy	1536	TGTGGTCAATTCATTAAGGCACTGATGGAATTTGCTGCTGTTTTCGCGAATCTCTTTG	1595
Db	1278	TGTGGTCAATTCATTAAGGCACTGATGGAATTTGCTGCTGTTTTCGCGAATCTCTTTG	1337
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## RESULT 12

AF438329 1517 bp mRNA linear PLN 13-NOV-2001  
 LOCUS Triticum aestivum isomylase precursor, mRNA, complete cds;  
 DEFINITION alternatively spliced.

ACCESSION AF438329

VERSION AF438329.1 GI:16905064

## KEYWORDS

SOURCE Triticum aestivum (bread wheat)

## ORGANISM

Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

## REFERENCE

1 (bases 1 to 1517)

Netrphan, S., Khandelwal, R.I. and Chibbar, R.N.

Characterization of isomylase transcripts produced during wheat

grain development and germination

Unpublished

2 (bases 1 to 1517)

Netrphan, S., Khandelwal, R.I. and Chibbar, R.N.

Direct Submission

Submitted (22-OCT-2001) Plant Biotechnology Institute, 110

Gymnasium Place, Saskatoon, SK S7N 0W9, Canada

Location/Qualifiers

## FEATURES

source

1. 1517

/organism="Triticum aestivum"

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Qy	61	TCGGCAGAGTGTGGCCCGCGCTGTCGAGGGGGCGAGAAAGTAGAGACGAGGGGAGG	120						
Db	238	TCGGCAGAGTGTGGCCCGCGCTGTCGAGGGGGCGAGAAAGTAGAGACGAGGGGAGG	297						
Qy	121	AGGACGAGCCGGTGGCGAGACAGGTACCGCGCTCGCGCGCGCTGACAGGGTGTCTGCCG	180						
Db	298	AGGACGAGCCGGTGGCGAGACAGGTACCGCGCTCGCGCGCGCTGACAGGGTGTCTGCCG	357						
Qy	181	GAATGCCCGCGCGCTGGCGGCCACCGGCTCGCGCGCGGGGTCAATTTGCCCGTCTATT	240						
Db	358	GAATGCCCGCGCGCTGGCGGCCACCGGCTCGCGCGCGGGGTCAATTTGCCCGTCTATT	417						
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DEFINITION	Oryza sativa mRNA for isoamylase, partial cds.			
ACCESSION	AB015615			
VERSION	AB015615.1	GI:3252793		
KEYWORDS	isoamylase.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Ehrhartoideae; Oryzaceae; Oryza.			
REFERENCE	1			
AUTHORS	Fujita, N., Kubo, A., Francisco, P.B. Jr., Nakakita, M., Harada, K., Minaka, N. and Nakamura, Y.			
TITLE	Purification, characterization, and cDNA structure of isoamylase from developing endosperm of rice			
JOURNAL	Planta	208 (2), 283-293 (1999)		
MEDLINE	99266133			
PUBMED	10333591			
REFERENCE	2 (bases 1 to 2288)			
AUTHORS	Nakamura, Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (17-JUN-1998) Yasunori Nakamura, National Institute of			
	Agrobiological Resources, Department of Plant Physiology; 2-1-2			
	Kannondai, Tsukuba, Ibaraki 305-8602, Japan			
	(E-mail:nakayn@affrc.affrc.go.jp, Tel:81-298-38-8382,			
	Fax:81-298-38-8347)			
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## ORIGIN

Query Match 36.7%; Score 1101.2; DB 8; Length 2288;  
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Db 2193 CAT 2196

RESULT 14  
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DEFINITION Sequence 16 from Patent WO9914314.  
ACCESSION AX031277  
VERSION AX031277.1 GI:10278607  
KEYWORDS  
SOURCE Aegilops tauschii  
ORGANISM Aegilops tauschii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Aegilops.

REFERENCE 1  
AUTHORS Li, Z., Morell, M. and Rahman, S.  
TITLE Regulation of gene expression in plants  
JOURNAL Patent: WO 99/4314-A 16 25-MAR-1999;  
GOODMAN FIELDER LTD (AU); LI ZHONGYI (AU); MORELL MATTHEW (AU);  
RAHMAN SADEQUER (AU); UNIV AUSTRALIAN (AU); COMMW SCIENT IND RES  
ORG (AU); GROUPE LIMAGRAIN PACIFIC PTY L (AU)  
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## RESULT 15

AR427894  
LOCUS AR427894 2700 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 15 from patent US 6639126.  
ACCESSION AR427894  
VERSION AR427894.1 GI:40186914

## KEYWORDS

Unknown.

## SOURCE

Unknown.

## ORGANISM

Unclassified.

1 (bases 1 to 2700)

Sewalt,V.J.H. and Singletary,G.W.

Production of modified polysaccharides

Patent: US 6639126-A 15 28-OCT-2003;

Location/Qualifiers

1..2700

source

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Query Match 33.6%; Score 1008; DB 6; Length 2700;  
Best Local Similarity 65.9%; Pred. No. 3.1e-187;  
Matches 1888; Conservative 0; Mismatches 345; Indels 633; Gaps 4;

Qy 79 CGGTGTGTCAGCGCGCAGCAGAGGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138  
Db 233 CGGTGCGCGCGCGGTGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 292  
Qy 139 AGGACAGGTACCGCTCGCGCGCGCTGACAGGGTCTCGCGCGGAATCCCGCGCGCTGG 198  
Db 293 AGGAGAGGTTCCGCTGGCGCGCGCTGCGCGGTCTCGCGGGAAATGCCCGCGCGCTCG 352  
Qy 199 GCGCCACGCGCTCGCGCGCGGTCAATTCGCGGTCTATTCGCGGAGGAGGAGGAGGAGG 258  
Db 353 GCGCCACGCGCTCGCGCGCGGTGTCAATTCGCGGTCTACTCGCGGTCTCTCTCGCGGT 412

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QY	319	GTTCATCAGCTTTGCGTGGCGCGCGCCCTTTTGGGCGCTGCAATTTAAGTTTGTGA	378	QY	1396	ATTGATGATCAGCAATGACCAATTTCTTGAGCGCTCAAGCTCAITTCCTGAAGCATGG	1455
Db	450	-----	449	Db	1453	ATTGATGATCAGCAATGACCAATTTCTTGAGCGCTCAAGCTCAITTCCTGAAGCATGG	1512
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QY	439	CGAGCGGGAACGTGTGGCTGCTTCAATCGAAGG---CGAGCTGCAACAATGCTTTAC	495	QY	1516	AATGGAAGTACCGGACATTTGTGGCTCAATTTCAATTAAGGCACTGATGGATTTCTGCT	1575
Db	493	CGAAGCGGAACGTGTGGCTGCTTCAATCGAAGG---CGAGCTGCAACAATGCTTTAC	552	Db	1573	AATGGAAGTACCGGACATTTGTGGCTCAATTTCAATTAAGGCACTGATGGATTTCTGCT	1632
QY	496	GGGTACAGTTTCAGCGGACCTTTGCTCCTCACTGCGGCACTACCTTTGATTTTCAAT	555	QY	1576	GGTTTTGCGAATGCTTTGTGGAAGTCCACACTATACCAGGTAAAGTTGTGGCAATACT	1635
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Db	853	GGTCTGTGTCAAAAGCTTGACCACTTAAAGGAACTTGGAGTGAATCTATAGAGCTAATG	912	Db	1672	-----	1671
QY	856	CCCTGCCATGATTTCAAGAGCTGGAGTACTCAACCTCTTCTTCCAGATGAATTTTGG	915	QY	1936	TCATAGTTAAGTTGCTTTTCTGTAAAGAAAGGAAACGACTTCATACTTTCTATCGGTGC	1995
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QY	916	GGATATTCTACCAATACTTTTCCCAATGACAAGATACATCAGCGCGGATATAAA	975	QY	1996	TAACCTAGCTCGATGTATATTATTGTAAGATGAATGCAAAATTTAATTTGTGCGAATAATTG	2055
Db	973	GGATATTCTACCAATACTTTTCCCAATGACAAGATACATCAGCGCGGATATAAA	1032	Db	1672	-----	1671
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Db	1273	GAAATTTATAGTGGATGCTTGAGATCTGGGTAAACAGAAATGCTGATGTTGATGTTTCGT	1332	Db	1826	GTGGGAGGAGGAGAAATTTGCAAGTGTCTGCAAGTCCGAAAGTAAAGGAGGAGGAGTGC	1885
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Search completed: August 9, 2004, 20:03:06  
Job time : 11423 secs

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3	1000	33.4	2112	2	AAx76375	Zea mays
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5	989	33.4	2715	6	AAx42890	Maize sug
6	673.2	22.5	2706	2	AAx27061	S. tubero
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9	613.2	20.5	2806	2	AAx27066	Original
10	575.4	19.2	2133	2	AAx96754	S. tubero
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13	405.8	13.5	1663	2	AAx33462	Potato is
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15	189.8	6.3	10439	6	AAx47817	Alternati
16	189.8	6.3	11779	6	AAx42891	Maize sug
17	188.8	6.3	501	6	AAx42926	Maize sug
18	183	6.1	4745	6	ABx54601	Synschoco
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Db 1561 GATGGATTGCTGGTGGTTTGGCGAATGTCITTTGTGGAGTCCACACCTATACAGGTA 1620  
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RESULT 2  
AA34654

ID AAX34654 standard; cDNA; 1706 BP.

XX AAX34654;

XX AC

XX 17-OCT-2003 (revised)

DT 05-JUL-1999 (first entry)

DT

XX

XX Partial cDNA for hexaploid wheat DBE.

XX

XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;

KW starch branching enzyme; starch soluble synthase; debranching enzyme;

KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;

KW grain softness protein 1; bacterial isoamylase; glycogen synthase;

KW WBE I-D4 gene; ss.

XX

XX Aegilops tauschii.

OS

XX

XX Key

XX Location/Qualifiers

FT CDS

FT 1..1704

FT /\*tag= a

FT /note= "partial DBE; the attr and stop codons are not

FT indicated"

XX

XX WO9914314-A1.

XX

XX 25-MAR-1999.

XX

XX 11-SEP-1998; 98WO-AU0000743.

XX

XX 12-SEP-1997; 97AU-00009108.

XX

XX 20-MAR-1998; 98AU-00002509.

XX

XX (CSIR ) COMMONWEALTH SCI &amp; IND RES ORG.

XX (AUSU ) UNIV AUSTRALIAN NAT.

XX (GOOD-) GOODMAN FIELDER LTD.

XX (LINA-) GRP LINAGRAIN PACIFIC PTY LTD.

XX

XX Li Z, Morell M, Rahman S;

XX

XX WPI; 1999-229525/19.

XX F-PSDB; AAY06918.

XX

XX New isolated cereal plant enzyme genes used for, e.g. expression of

PT antisense sequences of granule bound synthase.

XX

XX Claim 47; Page 100-102; 171pp; English.

XX

XX The invention relates to a novel enzyme of starch biosynthetic pathway in

XX a cereal plant, where the enzyme is selected from starch branching enzyme

CC

CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme  
 CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of  
 CC rice or maize. The methods and products can be used for targeting  
 CC expression specifically to the endosperm of the seeds of cereal plants  
 CC such as wheat or barley. They can be used for the expression of e.g.  
 CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.  
 CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial  
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be  
 CC used for modifying the characteristics of starch produced by a plant. The  
 CC present sequence represents the wheat DBE partial cDNA sequence. (Updated  
 CC on 17-OCT-2003 to standardise OS field)

XX  
 SQ Sequence 1706 BP; 467 A; 355 C; 415 G; 469 T; 0 U; 0 Other;

Query Match 35.8%; Score 1074.4; DB 2; Length 1706;  
 Best Local Similarity 74.9%; Pred. No. 6.6e-222;  
 Matches 1621; Conservative 0; Mismatches 16; Indels 527; Gaps 1;

QY 799 GCTGTGCGAAGCTTGACTATTTCGAAGAGCTTGGAGTTAAATGTAATTAATGCCCC 858  
 DB 1 GCTGTGCGAAGCTTGACTATTTCGAAGAGCTTGGAGTTAAATGTAATTAATGCCCC 60

QY 859 TGCCATGAGTTCAAGAGCTGGAGTACTCAACCTCTTCTCCAGATGAACCTTTGGGGA 918  
 DB 61 TGCCATGAGTTCAAGAGCTGGAGTACTCAACCTCTTCTCCAGATGAACCTTTGGGGA 120

QY 919 TATTTACCAATAAACTTTCTTTCACCAATGACAAGATACACATCAGCGGGGATAAAAAAC 978  
 DB 121 TATTTACCAATAAACTTTCTTTCACCAATGACGAGATACATCAGCGGGGATAAAAAAC 180

QY 979 TGTGGGCGTGATGCCATAAATAGATTCAAACTTTTGTAAAGAGAGCTCAAAACCGGGGA 1038  
 DB 181 TGTGGGCGTGATGCCATAAATAGATTCAAACTTTTGTAAAGAGAGCTCAAAACCGGGGA 240

QY 1039 ATTGAGGTGATCCTGGATGTTGCTTCAACATACAGCTCAGAGTAAATGAGATGTCCA 1098  
 DB 241 ATTGAGGTGATCCTGGATGTTGCTTCAACATACAGCTCAGAGTAAATGAGATGTCCA 300

QY 1099 ATATTATCAATTAAGGGGTCGATAATACATACATATATGTTGCACCCAAAGGGAGAG 1158  
 DB 301 ATATTATCAATTAAGGGGTCGATAATACATACATATATGTTGCACCCAAAGGGAGAG 360

QY 1159 TTTTATAACTATCTGCTGTGGGAATACCTTCACTGTAATCATCTGTGGTTCGTCAA 1218  
 DB 361 TTTTATAACTATCTGCTGTGGGAATACCTTCACTGTAATCATCTGTGGTTCGTCAA 420

QY 1219 TTCAATTTAGATTGTTTAAAGATACCTGGGTGACGGAATGATGTTGATGTTTTCGTTTT 1278  
 DB 421 TTCAATTTAGATTGTTTAAAGATACCTGGGTGATGGAATGATGTTGATGTTTTCGTTTT 480

QY 1279 GATCTTGATCCATAATGACAGAGGTTCCAGTCTGTGGGATCCAGTTAACTGTTATGGA 1338  
 DB 481 GATCTTGATCCATAATGACAGAGGTTCCAGTCTGTGGGATCCAGTTAACTGTTATGGA 540

QY 1339 GCTCCAATAGAAGTGATCATGATCACAAAGGACACCTCTTCTTACTCCACCACCTATT 1398  
 DB 541 GCTCCAATAGAAGTGATCATGATCACAAAGGACACCTCTTCTTACTCCACCACCTATT 600

QY 1399 GACATGATCAGCAATACCAATTTCTTGGAGGCGTCAAGCTCATGCTGAAGCATGGAT 1458  
 DB 601 GACATGATCAGCAATACCAATTTCTTGGAGGCGTCAAGCTCATGCTGAAGCATGGAT 660

QY 1459 GCAGGAGGCTCTATCAAGTAGTCAATTCCTCCTCACTGGAACTTTTGGTCTGAGTGGAT 1518  
 DB 661 GCAGGAGGCTCTATCAAGTAGTCAATTCCTCCTCACTGGAACTTTTGGTCTGAGTGGAT 720

QY 1519 GGGAAAGTACCGGACATTTGCTGCTCAATTCATTAAGGCACTGATGGAATTTGCTGGTGT 1578  
 DB 721 GGGAAAGTACCGGACATTTGCTGCTCAATTCATTAAGGCACTGATGGAATTTGCTGGTGT 780

QY 1579 TTTGCGCAATGCTTTTGTGGAAGTCCACACCTATACAGGTAGTTGTGGCAATCTTGT 1638  
 DB 781 TTTGCGCAATGCTTTTGTGGAAGTCCACACCTATACAGGTAGTTGTGGCAATCTTGT 1698

QY 1639 AAATGAGTTGAGTGAATGTCACTGGATTTTTTATATATATACCATGATGATACATCT 1698  
 DB 817 ----- 816

QY 1699 AAATATATAACAATCATAGTGTATGCATATGCAATTTGGCTAAGAAGTATTAGTGTATACA 1758  
 DB 817 ----- 816

QY 1759 CTAGTGTATATATATAGTTTAAACACCAACTTGCATGAAGGAACATAGGGCTTTCTA 1818  
 DB 817 ----- 816

QY 1819 GTTATCTTATTATTGTCGGTGAATAATCCACTGAAATAATCCAGCCATGTCAATTTT 1878  
 DB 817 ----- 816

QY 1879 TAGGGGGGAGAGAAACTATATTGATTTGCCCCCTAAAAAGAGCCATCTCAGAAATCA 1938  
 DB 817 ----- 816

QY 1939 TAGGTAAGTTGCTTTTCTGTAAAGAAAGAAACGACTTCATATCTTCTATCGGTGTAA 1998  
 DB 817 ----- 816

QY 1999 CTTAGCTCGATGATATTTTGTAGATGAATGCCAAATTTAATTTTGTCCGATAAATTTGATC 2058  
 DB 817 ----- 816

QY 2059 TGTATTCCAAATTTCTATTGTTGTTCTCTAGAATCAAAACAGTAACCTTGTATTGGC 2118  
 DB 817 ----- 816

QY 2119 ACTGCAACTTCTTATTGATTAAATCAGGCAGGAGGAACCTTTGGCACAGTATCAACT 2178  
 DB 817 ----- 816

QY 2179 TTGTATGTGCATGATGATTTTACATCTGGTGTATTTGGTAAACATATAATAAAGATACA 2238  
 DB 854 TTGTATGTGCATGATGATTTTACATCTGGTGTATTTGGTAAACATATAATAAAGATACA 913

QY 2239 ATTTACCAATTTGGGAGAACACAGAGATGAGAAATCAAACTTTAGCTTGGAAATTTGTG 2298  
 DB 914 ATTTACCAATTTGGGAGAACCAATAGATGGAATAATCAAACTTTAGCTTGGAAATTTGTG 973

QY 2299 GGGAGGAAGGAATTCGAAAGATTCTGTCAAAAGATTGAGGAAGAGGAGATGGCA 2358  
 DB 974 GGGAGGAAGGAATTCGAAAGATTCTGTCAAAAGATTGAGGAAGAGGAGATGGCA 1033

QY 2359 ATTTCTTTGTTTGTCTCATGTTTCTCAAGGAGTTCCAATGTTCTACATGGGTGATGAAT 2418  
 DB 1034 ATTTCTTTGTTTGTCTCATGTTTCTCAAGGAGTTCCAATGTTTCTACATGGGTGATGAAT 1093

QY 2419 ATGGCCACAAAAAGGGGGCAACCAATACATCTGCCATGATTTCTATGTCAATTAAT 2478  
 DB 1094 ATGGCCACAAAAAGGGGGCAACCAATACATCTGCCATGATTTCTATGTCAATTAAT 1153

QY 2479 TTCGTGGGATAAAAAGAAACAATCTCTGAGTTGCAACGATTTCTGCTGCTCATGACCA 2538  
 DB 1154 TTCGTGGGATAAAAAGAAACAATCTCTGAGTTGCAACGATTTCTGCTGCTCATGACCA 1213

QY 2539 AATTCCGCAAGGAGTGGAGGGTCTTGGCTTTGAGGACTTTTCCAAAGGGCAAGCGGTGC 2598  
 DB 1214 AATTCCGCAAGGAGTGGAGGGTCTTGGCTTTGAGGACTTTTCCAAAGGGCAAGCGGTGC 1273

QY 2599 AGTGGCATGTGTCATGAGCTTGGGAAGCTGATTTGGTCTGAGATAGCCGATTTCTTGGCT 2658  
 DB 1274 AGTGGCATGTGTCATGAGCTTGGGAAGCTGATTTGGTCTGAGATAGCCGATTTCTTGGCT 1333

QY 2659 TTTCCATGAAGATGAAGAGCAGGGCGAGATCTATGTGGCTTCAACACAGCCACTTAC 2718  
 DB 1334 TTTCCATGAAGATGAAGAGCAGGGCGAGATCTATGTGGCTTCAACACAGCCACTTAC 1393



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QY 1216 CAATTCATTGTAGATGTTTAAAGATACCTGGGTGAGGAAATGCAATGTTGATGTTTTCGT 1275
DB 1273 GAATTTATAGTGGATGCTTGCAGATACCTGGGTAAACAGAAATGCAATGTTGATGTTTTCGT 1332
QY 1276 TTTGATCTTGGCATCCATAATGACACAGAGGTTCCAGTCTGTGGATCCAGTTAAGCTGAT 1335
DB 1333 TTTGACCTTGCAATCTATACCTACAGAGAGTGCAGTCTATGGGATCCAGTTAATGTTGAT 1392
QY 1336 GGAGCTCCAAATGAGAGGTGACATGATCACAACAGGACACCTCTTGTACTCCACCACTT 1395
DB 1393 GGAAAGTCCAAATGGAAGGTGACATGATTACGACAGGACACCTCTTGTGTTGCCACCACTT 1452
QY 1396 ATTCACATGATCAGCAATGACCAATCTTGGAGCGTCAAGCTCAATGCTGAAGCATGG 1455
DB 1453 ATTGACATGATTAGCAATGACCAATCTTGGAAATGTCAAGCTCATGCTGAAGCATGG 1512
QY 1456 GATCAGAGAGCCCTCTATCAAGTAGTCAATTCCTCACTGGAATGTTTGGTCTGAGTGG 1515
DB 1513 GATCAGAGAGTCTCTATCAAGAGGTCAAGTTTCTCTCACTGGAACGTTTGGTCAAGTGG 1572
QY 1516 AATGGAAAGTACCGGACATGTCGCTCAATTCATTAAGGACATGATGATTTGCTGGT 1575
DB 1573 AATGGAAAGTATCGCATACCGTGCCTCAGTTTCATCAAGGACACAGATGGAATTTGCTGGT 1632
QY 1576 GGTTTTGGCGAATGCTTTTGGGAAGTCCACACCTATACCAGGTAAAGTTGTGGCAATACT 1635
DB 1633 GCTTTTGTGTAAGTCTTGTGGAAAGTCCACAGTTATC----- 1671
QY 1636 TGTAATGAGTTGAGTGAATGTCACCTGGATTTTATATATATACCAATGATGATACACA 1695
DB 1672 ----- 1671
QY 1696 TCTAAATATATAACATATAGTGTATGATATGCAATTTGGCTAAGAAATATTAGTGTAT 1755
DB 1672 ----- 1671
QY 1756 ACACCTAGTGTATATATAGGTTTAAACACCACTTGCCAAATGAAGGAACATAGGCTTT 1815
DB 1672 ----- 1671
QY 1816 CTAGTTATCTTATTATTATTGTCGGTGAATTAATCCACTGAAATATCCAGCCATGTCATT 1875
DB 1672 ----- 1671
QY 1876 TTTTAGGGGGGAGAGAAACTATATTGATTGTCGCCCTTAAAGAGCCATCTCAGAAAT 1935
DB 1672 ----- 1671
QY 1936 TCATAGTAAAGTCTGTTTCTGTAAAGAAAGAAACGACTTCATCTTCTATCGGTGC 1995
DB 1672 ----- 1671
QY 1996 TAACTTAGTCGATGATATTGTTAGATGAATGCCAAATTTAATTTGTCGATAATTG 2055
DB 1672 ----- 1671
QY 2056 ATCTGTTATTCACAAATTTCTATTGTTGTTTCTCTAGAAATCAAAACAGTAACCTTGTATT 2115
DB 1672 ----- 1671
QY 2116 GGCACTGCAACTCTTATTGTTAATCAGCGAGAGGAAGAAACCTTGGCAAGTATCA 2175
DB 1672 -----CAGCGAGGGGAGGAAGCCCTTGGCAAGTATCG 1705
QY 2176 ACTTTGTTATGTCACATGATGATTACATGCTGCTGATTTGGTAAACATATAAAGAAGT 2235
DB 1706 GCTTTGTTATGTCACACAGTGAATTTACATGCTGCTGATTTGGTCAACATAGCAAGT 1765
QY 2236 ACAATTTACCAATGGGAGACACACAGATGAGAAATCAATCTTAGCTGAATTT 2295
DB 1766 ACAACTTGTCAAATGGTGAAGACTTCAGATGGGAAATCATATCTTAGCTGAATTT 1825

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QY 2296 GTGGGAGGAGAGAAATTCGCAAGATTGTCCTGTCAAAAGATTGAGGAAGGCGAGATGC 2355
DB 1826 GTGGGAGGAGAGAAATTCGCAAGTTGTCAGTCCGAGAAATTAAGGAAGAGGCAATGTC 1885
QY 2356 GCAATTTCTTTGTTGTTCTCATGTTTCTCAAGAGATTCCAAATGTTCTACATGGGTGATG 2415
DB 1886 GCAATTTCTTTGTTGTTCTTATGTTTCTCAGGAGTTCCAAATGTTCTACATGGCGATG 1945
QY 2416 AATATGGCCACACAAAAGGGGGCAACAATACTGCTGCAATGATCTTATGTCAATT 2475
DB 1946 AATATGGTCAACAAGGAGGAGCAACAATACTGCTGCAATGATCTTATGTCAATT 2005
QY 2476 ATTTTTCGCTGGGATATAA---AAGAAACAATACTCTGAGTTGCACCGATTCTGCTGCCTCA 2532
DB 2006 ATTTCCGTTGGATTAAGAGGAAGAAACAATCTCTGATTGTACAGATTCTGCCGTCTCA 2065
QY 2533 TGACCAAAATTCGCAAGAGTGCAGAGGTCTTGGCCCTTGAGGACTTCCAAACGGCCAAAC 2592
DB 2066 TGACCGAATTCGCAAGAGATGTGAATCTCTTGGCCCTTGAGGACTTCCGACTTCAGAAC 2125
QY 2593 GCCTCAGTGGCATGTTGATCAGCTCGGAAGCCTGATTTGGTCTGAGATAGCCGATTCG 2652
DB 2126 GGTGAAATGGCAGGTGATCAGCCCGGGAAGCCTGACTGGTCAGAGCAAGCCGATTCG 2185
QY 2653 TTGCTTTTCCATGAAAGATGAAAGACAGAGGCGGAGATCTATGTGGCCCTTCAACACCGACC 2712
DB 2186 TTGCTTTTCCATGAAAGACGAAACCAAGCGAGATCTACGTGGCCCTTCAACACCGAGTC 2245
QY 2713 ACTTACCGCGCTGTTGAGCTCCAGAGCGCGCAGGCGCGGTGGGAACCGGTGGTGG 2772
DB 2246 ACCTTCCGCTGTTGTTGGGCTTCCAGAGCGCTCTGGGTTCCGATGGGAGCCGCTGGTGG 2305
QY 2773 ACACAGGAAGCAGCAGCACCATACGACTTCCCTCACCGAGACTTACCTGATCGCGCTCTCA 2832
DB 2306 ACACCGGAAGAGGACCATATGACTTCCCTCACCGATGGCTCCAGATCGTCTGTCTCA 2365
QY 2833 CATACACAGTTCGCAATTCCTTACTCTCAACCTCTACCCCATGCTCAGTACTCAT 2892
DB 2366 CCGTACAGTTCCTCTCATTTCTCACTCAATCTCTATCTCTATCTCTATGCTCAGCTACTCCT 2425
QY 2893 CGGTACCTCTAGTATGCGCCCTGATGTTTGAGAGACCAATATATA 2938
DB 2426 CAATCATCTCTGATTGGCCCTGATGCTGAAAAGAGCAGATACA 2471

RESULT 4
AAD47816
ID AAD47816 standard; cDNA; 2712 BP.
XX
AC AAD47816;
XX
DT 24-FEB-2003 (first entry)
XX
DE Alternative version of maize sugary1 (SUI) cDNA.
XX
KW Maize; starch debranching enzyme; sugary1; industrial application; SUI;
KW starch processing industry; gene; ss.
XX
OS Zea mays.
XX
FH Key
FT CDS
FT 1..2457
FT /tag= a
FT /product= "Alternative version of SUI protein #1"
FT /note= "No start codon"
FT /partial
XX
PN US6410716-B1.
XX
PD 25-JUN-2002.
XX
PF 24-FEB-1999; 99US-00256741.
XX

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Db	1672	-----	1671
Qy	1816	CTAGTTATCTTATTATTATTGTCGGTGAATAATCCACTGAAAAATCCAGCCATGTCA	1875
Db	1672	-----	1671
Qy	1876	TTTTAGGGGGGAGAGAAACTATATTGATTTGCCCCCTTAAAGAGCCATCTCAGAA	1935
Db	1672	-----	1671
Qy	1936	TCATAGGTAAAGTTGCTTTTCTGTAAAGAAAGAAACGACTTCATCTTCTATCGGTGC	1995
Db	1672	-----	1671
Qy	1996	TAACTTAGCTCGATGTATATTTGTAAGATGAATGCCAAATTTAATTTGTCCGATAA	2055
Db	1672	-----	1671
Qy	2056	ATCTGTTATTACAAAATTTCTATTGGTTTCTCTAGAAATCAAACCAAGTAAC	2115
Db	1672	-----	1671
Qy	2116	GGCACTGCAACTTCTTATTGATTAAATCAGGCAGGAGGAAGAAACCTTGGCAGAT	2175
Db	1672	-----	1705
Qy	2176	ACTTTGTATGTGCATGATGGATTTACATGGCTGATTTTGGTAAATATATAAGAA	2235
Db	1706	GCTTTGTATGTGCACAGATGGATTTACATGGCTGATTTGGTCACATACAATAG	1765
Qy	2236	ACAATTTACCAATGGGAGAAACAACAGAGATGGAGAAATCAAAATCTTTAGCT	2295
Db	1766	ACAATTTGTCAATGGTGAGACTTTCAGAGATGGGAAATCATATCTTTAGCT	1825
Qy	2296	GTGGGAGGAAGGAATTCGCAAGATTGTCTCAAAAGATTGAGAAAGGAGATGC	2355
Db	1826	GTGGGAGGAAGGAATTTGCAAGTCTGTCAAGATTAAAGGAAGGCAATGC	1885
Qy	2356	GCAATTTCTTTGTTGCTCATGGTTTCTCAAGGAGTTCCAAATGTTCTCATCGGT	2415
Db	1886	GCAATTTCTTTGTTGTTCTTAAGTTTCTCAGGAGTTCCAAATGTTCTCATCGG	1945
Qy	2416	AATATGCCACAAAAAGGGGCAACAAATACATCTGCCATGATTTCTATGTCAAT	2475
Db	1946	AATATGTCACACAAAGGGAGGAACAACAATACGTACTGCCATGACCATTTATGT	2005
Qy	2476	ATTTTCCTCGGATAAAA---NAGAAATACTCTGATTTGCAACCGATCTGCTGC	2532
Db	2006	ATTTCCCTTGCGATTAAGAGGAAGAAATCTCTGATTTGTACAGATCTGCGGT	2065
Qy	2533	TGACCAAAATCCGCAAGAGTGCAGAGGTCTTGCCCTTGAGGACTTTCCAAAGCC	2592
Db	2066	TGACCGAATTCGCAAGATGTGAATCTCTTGCCCTTGAGGACTTCCGACTTCAG	2125
Qy	2593	GGCTGAGTGGCATTGTCTACAGCTGGGAAGCCTGATTTGGTCTGAGATPAGCG	2652
Db	2126	GGTTGAATGGCATCGGTTCATCAGCCCGGAAGCCTGACTGGTCAGAGGCAAG	2185
Qy	2653	TTGCTTTTCCATGAAAGATGAAAGACAGGGCGAGATCTATGTGGCTTCAAC	2712
Db	2186	TTGCTTCCATGAAGGACGAACCAAGGCGAGATCTACGTGGCTTCAACACAG	2245
Qy	2713	ACTTACCGGCGTTGTTGACTCCAGAGCGGACGGCCGGTGGGAACCGGTGG	2772
Db	2246	ACCTTCGGTGGTTGTTGGCTTCCAGAGGGCTCTGGGTTCCGATGGGAGCCG	2305
Qy	2773	ACACAGGCAAGCAGCACCATACGACTTCTCACCGACGACTTACCTGATCGCG	2832
Db	2306	ACACCGGCAAGGAGGACCAATATGACTTCTCACCGATGGCTGCCAGATCG	2365
Qy	2833	CCATACACCAAGTTCTCGCATTTCTCTACTCCAACTCTACCCCATGCTCAG	2892

Db	2366	CGCTGTACAGTCTCTCATTTCTCCTCAACTCCAATCTCTATTCCTATGCTAGTACTCTCT	2425
Qy	2893	CGGTCACTCTAGTAGTATTCGGCCCTGATGTTTGGAGAGACCAATATATA	2938
Db	2426	CCATCATCTTGTTATTCGGCCCTGATGTTCTGAAAGAGCAGATACA	2471
RESULT 5			
AD42890			
ID	AD42890	standard; cDNA; 2715 BP.	
XX			
AC	AD42890;		
XX			
DT	24-FEB-2003	(first entry)	
DE			
XX			
DE	Maize sugary1 (SU1) cDNA.		
XX			
KW	Maize; starch debranching enzyme; sugary1; industrial application; SU1;		
KW	starch processing industry; gene; ss.		
XX			
OS	Zea mays.		
XX			
Key	Location/Qualifiers		
FT	88..2454		
CDS	/*tag= a		
FT	/product= "SU1 protein"		
FT	/note= "No stop codon"		
FT	/partial		
XX			
XX	US6410716-B1.		
PN			
XX			
PD	25-JUN-2002.		
XX			
PF	24-FEB-1999;	99US-00256741.	
XX			
PR	24-MAR-1995;	95US-00410784.	
XX			
PA	(IOWA ) UNIV IOWA STATE RES FOUND INC.		
XX			
PI	Myers AM, James MG;		
XX			
XX	WPI; 2002-616514/66.		
DR	P-PSDB; AAE25988.		
DR			
XX			
PT	Novel starch debranching enzyme protein sugary1 or its polypeptide		
PT	fragment useful as replacement for bacterial and fungal enzymes currently		
PT	used in starch processing industry.		
XX			
XX	Claim 20; Col 31-38; 75pp; English.		
PS			
XX			
CC	The invention relates to maize starch debranching enzyme, sugary1 (SU1)		
CC	and nucleic acid molecules encoding such proteins. SU1 sequences are used		
CC	as a replacement for the bacterial and fungal enzymes currently used in		
CC	the starch processing industry and as immunogens to raise antibodies		
CC	against SU1. Polynucleotides of the invention are useful as markers for		
CC	identification of specific corn varieties, for the development of corn		
CC	varieties with starch properties tailored for specific industrial		
CC	applications. The present sequence is maize SU1 cDNA. Note: This sequence		
CC	is stated to be the same as that shown as SEQ ID NO:1 (AAD47816) in		
CC	figure 1 of the specification. However the sequences differ		
XX			
SQ	Sequence 2715 BP; 637 A; 645 C; 747 G; 686 T; 0 U; 0 Other;		

	Query Match	33.0%	Score 989;	DB 6;	Length 2715;
	Best Local Similarity	65.7%;	Pred. No. 2,1e+203;		
	Matches 1883;	Conservative	0;	Mismatches 350;	Indels 634;
					Gaps 5;
Qy	79	CGGTGTCGAGGCGGCGACGAAGTACAGACACGAGGGAGGACGACGAGCGGTGCGCG	138		
Db	235	CCGTGCGCGAGCGGTCTACGCGGAGGAGACGACGACGACGACGAGGAGGTGCGCG	294		
Qy	139	A-GGACAGGTACGCGTCCGCGCGCGGTGTCAGGGTGTCTCCCGGAAATGCCCGCCCGCGTG	197		

295 AGGAGAGGTTCCGCTGGGCGCGCGTGCCTGGCGGTGCTCGCGGAATGCTCCGCGCGCTC 354  
198 GGGCCACCGCGCTCGCGGCGGGTCAATTTGCGCGTCTATTCCGCGGAGCAACGCGC 257  
355 GCGCCACCGCGCTCGCGGCGGGTCAACTTGCCTCTACTCCAGCGGTGCTCCGCC 414  
258 GCGCGCTCTCCCTCTTACGCCAAGAAGATCTCAAGCGGTGGGGTTCCTCCCGAGTAG 317  
415 GCGTCGCTAGCGCTCTTCGCTCCCGCGGACCTCAAGGC----- 452  
318 AGTTCATCAGCTTTGCGTGGCGCGCGCGCGCTTTTGGCCCTGCAATTAAGTTTGT 377  
453 ----- 452  
378 ACTGGGCAATGCTGCAGGATAGGTTGACCGAGGAGTTCCTCCTGCACCCCTGATGAA 437  
453 ----- GATAGGGTGAACGAGGAGTGGCCCTCGATCCCTGCTCAA 494  
438 TCGAACCGGGAACGTGTGGGATGCTTCATCGAAGG---CGAGCTGCACAAATGCTTTA 494  
495 CCGAACCGGGAACGTGTGGACGTGTTTCATCCACGGGACGAGTGCACGGCATGCTCTG 554  
495 CGGTTACAGGTTCCACGCGACCTTTGCTCCTCACTGGGCGACCTACCTTGATGTTCCAA 554  
555 CGGATACAGGTTGATGGCTGTTTCGCCCTTGAGCGCGACGACTACGATGTGCCAA 614  
555 TGCTGCTGGATCTTATGCTAAGCAGTGAATAGCCGAGGAGTATGCTGTCCAGC 614  
615 CGTTGCTGGATCCATACGCTAAGGAGTGTAAAGCCGAGGTGAATATGCTGTGCTGC 674  
615 GCGTGTGTAACAAATTGCTGGCTCAGATGGCTGGCATGATCCCTCTTCATATAGCAGTT 674  
675 GCCTGGTGGTATGTTGGGCTCAATGGCTGGTATGATCCCTCTTCCTATATAAGTT 734  
675 TGATTGGGAGGCGACCTACCTCTAAGATATCTCAAAAGGACCTGGTGAATATAGAT 734  
735 TGATTGCAAGTCACTACCTTGGGTACCATCAGAGGACCTTGTCTATATGAAT 794  
735 GCACTTGGCTGGATTCAGAGCATGATTCAGCAATGTAGCAATCCGGGTACTTTTCAT 794  
795 GCAATTGGTGGATTCAGAGCACTCAAGCAGACAAACACCCAGGAACTTACAT 854  
795 TGGAGCTGTGCGAAGCTTGACTATTGGAAGGAGCTTGGAGTTAATGTATGCAATTAAT 854  
855 TGGTGTGTGTCAGAGCTTGACATCTAAGGAACTTGGAGTGAACCTGTATAGAGCTAAT 914  
855 GCCCTGCCATGAGTTCAACGAGCTGGAGTACTTCAACCTCTTCTTCCAAGATGAACCTTTG 914  
915 GCCCTGCCATGAGTTCAATGAGCTAGAGTACTTCAAGCTCTCTTCCGAGATGAACCTTCG 974  
915 GGGATATCTACCAATAACTTTTTCACCAATGACAGATACACATCAGCGCGGATAAA 974  
975 GGGATATTCACAAATAAATTTTTCTCACCATGGCAAGATATCTTCAAGTGGCATAAG 1034  
975 AAACTGGGCGGTGATGCCATAAATGAGTTCAAAACTTTTGTAGAGAGGCTCACAAACG 1034  
1035 AGACTCTGGATGTGGTCCATAAATGAATTTAAGCTTTTGTAGGGAGGCGCCACAAACG 1094  
1035 GGGAAATTGAGGTGATTCCTGGATGTGCTTCAACCATACAGCTAGAGGTAAATGAGATGG 1094  
1095 GGGAAATTGAGGTGATTCAGATGTGCTTCAATCAATACAGCTGAAGGTAAATGAGAAAG 1154  
1095 TCCCAATATATCAATTAAAGGGGTGATAATACATACATATATATGCTTCGACCCCAAGGG 1154  
1155 CCCAATATATCTTTAGGGGATAGATATATAGTACATATCTACATGCTTGACCTAAGGG 1214  
1155 AGAGTTTATATCTGCTGCTGGGAATACCTTCAACTGTAAATCATCCTGTGGTTCG 1214  
1215 AGAGTTTATATATCTGCTGGGAATACCTTCAATGTAAATCATCCTGTAGTCCG 1274  
1215 TCANNTCAATGTAGATTTTAAAGATCTGGGTGACCGAAATGCAATGCTGTTGATGTTTCG 1274  
1275 TGAATTTATAGTGATTGCTTTGAGATCTGGGTAAACAGAAATGATGCTGTTGATGTTTCG 1334

1275 TTTTGTCTTTCGATCCATAATGACACAGAGTTCCAGTCTGTGGATCCAGTTAAAGTGT 1334  
1335 TTTTGACCTTTGCTCTATCTACTGACAGAGGATGCGAGTCTATGGGATCCAGTTAATGT 1394  
1335 TGGAGCTCCAAATAGAAGGTGACATGATCACAAACAGGACACCTCTTGTACTCCACCACT 1394  
1395 TGGAAAGTCCAAATGGAAGGTGACATGATTAGCACAGGACACCTCTTGTGCCCCCACT 1454  
1395 TATTGACATGATCAGCAATGACCCAAATTTCTTGGAGGCGTCAAGCTCATTTGCTGAAGCATG 1454  
1455 TATTGACATGATTAGCAATGACCCAAATTTCTTGGAAATGTCAAGCTCATTTGCTGAAGCATG 1514  
1455 GGATGAGGAGGCGCTCTATCAAGTAGGTCAATTTCCCTCACTGGAATGTTTGGTCTGAGTG 1514  
1515 GGATGAGGAGGCTCTCTATCAAGAGGTGAGTTTCTCTCACTGGAACGTTTGGTCAGAGTG 1574  
1515 GAATGGAAAGTACCGGACATTTGTCGTCATATTAAGGACATGATGATTTGCTGG 1574  
1575 GAATGGAAAGTATCGGATACCGTGCATCAAGGACAGATGGAATTTGCTGG 1634  
1575 TGGTTTGGCGGAATGCTTTTGGGAAGTCCACACCTATACCAAGTAAAGTTGTGGCAATAC 1634  
1635 TGCCTTTGCTGAATGCTTATGCTATGTTGGAAGTCCACAGTTATAC----- 1674  
1635 TTTGAAATGAGTTGAGTGAATGTCACCTGGATTTTTTATATATATACCAATGATGATACAC 1694  
1675 ----- 1674  
1695 ATCTAAATATATAACATCATAGTGTATGCTATGCTTGGCTAAGAGTATTAGTGT 1754  
1675 ----- 1674  
1755 TACACTAGTGTATATATAGGTTTTTAACACCCCACTTGCCAATGAAGGAACATAGGGCTT 1814  
1675 ----- 1674  
1815 TCTAGTTATCTTATTTATTTGTCGGTGAATTAATCCACTGAAATAATTCAGCCATGTCAT 1874  
1675 ----- 1674  
1875 TTTTGGGGGGGAGAGAACTATATTGTTGCCCCCTAAAAGAACCATCTCAGAA 1934  
1675 ----- 1674  
1935 TTCATAGTGAAGTGTGCTTTCTGTAAAGAAAGAAACGACTTCATATCTTCTATCGGTG 1994  
1675 ----- 1674  
1995 CTAACTTAGCTCGATGTATTTTGTAAAGTGAATGCCAAATTTAATTTTGTTCGATAATTT 2054  
1675 ----- 1674  
2055 GATCTGTTATTCACAAATTTCTATTTGTTTCTCTAGAAATCAAAACCAGTAACCTTTTAT 2114  
1675 ----- 1674  
2115 TGGCACTGCAACTCTTATTTGATTAATCAGGACAGGAGGAAGAAACCTTTGGCACAGTATC 2174  
1675 ----- CAGGACAGGGGGGAGGAGCCCTTTGGCACAGTATC 1707  
2175 AACTTTGTATGTGCACATGATGCAATTTACACTTGGCTGATTTGGTAACATATATAAAGAG 2234  
1708 GCGTTTGTATGTGCACATGATGATTTACACTGGCTGATTTGGTCAATACATACATAGCAAG 1767  
2235 TACAAATTTACAAATGGGAGAAACACAGAGATGAGAAATAATCAAACTTTAGCTGGAAAT 2294  
1768 TACAACTTTGTCAAATGGTGGAGACTTCAGAGATGGGAAATAATCAATACTTTAGCTGGAAAT 1827  
2295 TGTGGGAGGAGGAGAAATTCGCAAGATTTGCTGTCAAAAGATTGAGGAAGGAGGAGATG 2354  
1828 TGTGGGAGGAGGAGAAATTTGCCAAGTCTGTGAGTCCGAAATTAAGGAAGGAGGAAATG 1887

QY 2355 CGCAATTCCTTTGTTGTTCTCATGTTCTCAAGGAGTTCCAAATGTTCTACATGGGTGAT 2414  
 Db 1888 CGCAATTCCTTTGTTGTTCTCATGTTCTCAAGGAGTTCCAAATGTTCTACATGGGTGAT 1947  
 QY 2415 GAATATGCCACACAAAGAGGGGCAACAACAATACATACATGCTGCAATGTTCTATGTCAT 2474  
 Db 1948 GAATATGGTCACAAAGGAGGGCAACAACAATACATACATGCTGCAATGTTCTATGTCAT 2007  
 QY 2475 TATTTCCGCTGGGATAAAA---AGAAACAATATCTCTGAGTTGACCAAGTTCTGTCGCTC 2531  
 Db 2008 TATTTCCGCTGGGATAAAA---AGAAACAATATCTCTGAGTTGACCAAGTTCTGTCGCTC 2067  
 QY 2532 ATGACCAAAATCCCAAGGAGTGGAGGGCTTGGCCCTTGAGGACTTTCCAAAGGGCAAA 2591  
 Db 2068 ATGACCGAATCCCAAGGAGTGGAGGGCTTGGCCCTTGAGGACTTTCCAAAGGGCAAA 2127  
 QY 2592 CGGCTGACGTCGATGTCATACGCTCGGAGGCTGATTTGGTCTGAGAAATACCGGATTC 2651  
 Db 2128 CGGTTGAAATGGCAGCGTCTATCAGCCGGGAGGCTGATTTGGTCTGAGAAATACCGGATTC 2187  
 QY 2652 GTTGCCTTTTCCATGAAGATGAAGACAGGGGAGATCTATGTCGCTTCAACACGAC 2711  
 Db 2188 GTTGCCTTTTCCATGAAGATGAAGACAGGGGAGATCTATGTCGCTTCAACACGAC 2247  
 QY 2712 CACTTACCGGCGTGTGTTGAGCTCCAGAGCGCGCGGCGCGGTGGGAAACGGTGGTG 2771  
 Db 2248 CACCTTCGGGTGGTGTGGGCTTCCAGAGCGCTCGGTCCGATGGGAGCGGTGGTG 2307  
 QY 2772 GACACAGGCAAGCAGACACATACGACTTCTCCACGAGCTTACCTGATCGGCTCTC 2831  
 Db 2308 GACACCGCAAGGAGGACCATATGACTTCTCCACCGATGGCCCTGCCAGATCGTGTGTC 2367  
 QY 2832 ACCATACACAGTCTCGCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2891  
 Db 2368 ACCGCTACCAAGTTCT 2427  
 QY 2892 TCGGTCTATCT 2938  
 Db 2428 TCCATCATCT 2474

## RESULT 6

AA27061  
 ID AA27061 standard; DNA; 2706 BP.

XX AC AA27061;

XX DT 21-MAY-1999 (first entry)

XX DE S. tuberosum isoamylase clone 15 coding sequence.

XX KW Isoamylase clone; potato; branched polysaccharide synthesis; amylopectin;  
 starch modification; debranching activity; ss.

XX OS Solanum tuberosum.

XX FN WO9906575-A1.

XX PD 11-FEB-1999.

XX PF 30-JUL-1998; 98WO-GB002280.

XX PR 31-JUL-1997; 97GB-00016185.

XX PA (PLAN-) PLANT BIOSCIENCE LTD.

XX PI Edwards EA, Smith AM, Martin CR, Bustos Guillen R;

XX DR WPI; 1999-153803/13.

XX DR P-PSDB; AAY00869.

XX PT New nucleic acid from potato encoding starch debranching enzyme with  
 isoamylase activity - and related vectors, transformed cells and plants.

PT proteins and antibodies, used to generate starch with altered properties,  
 PT for use in foods, as thickeners etc.  
 XX  
 PS Claim 3; Fig 2; 78pp; English.  
 XX This sequence encodes a Solanum tuberosum isoamylase of the invention.  
 CC Fragments of the isoamylase coding sequence are used to identify and  
 CC clone isoamylases from other plant species, by standard hybridisation or  
 CC amplification methods. Expression of the isoamylase DNA in host cells is  
 CC used to produce the isoamylase which is used: (i) to raise antibodies  
 CC (Ab) (for identification, isolation and localisation of isoamylases); and  
 CC (ii) for synthesis of branched polysaccharides. The DNA, proteins and Ab  
 CC (or related peptides) are used to alter the quality and quantity of  
 CC polysaccharides in a host cells, specifically to alter branching in  
 CC amylopectin. The modified starches produced are useful in human or animal  
 CC foods; as biodegradable plastic; as food or paint thickener; in starch-  
 CC coated films, paper and textiles; in mining explosives; in  
 CC pharmaceuticals and glues. Manipulation of debranching activity in a  
 CC plant allows control of starch properties, e.g. increased gel strength;  
 CC formation of paste rather than gel, changed physical characteristics etc  
 XX  
 SQ Sequence 2706 BP; 797 A; 492 C; 524 G; 792 T; 0 U; 1 Other;

Query Match 22.5%; Score 673.2; DB 2; Length 2706;

Best Local Similarity 69.4%; Pred. No. 3.4e-135;

Matches 937; Conservative 0; Mismatches 398; Indels 15; Gaps 1;

QY 395 AGGATAGGTCACGAGGAGGTCCTCCCTGACCCCTGATCAATCGGACCGGACGCTGT 454

Db 425 AGAAGAGAGTACCGAGCAAAATTTCTGGATCTCTAGCTAATAAACTGGAGATGAT 484

QY 455 GGCATGTCTTCATCAAGGCGAGTCGACAAACATGCTTTACGGGTACAGGTTCCAGCGCA 514

Db 485 GGCATGTGTCTTAAAGGAGATTTTGAGATATGCTATATGGCTACAAATTCGATGGGA 544

QY 515 CTTTTGCTCTCACTGCGGGCACTACCTTGATGTTTCAATGTCGTGGTGAATCTTATG 574

Db 545 AATTCGTCTTGAAGAGGACACTACTTTGACTCTTCGAGATAGTGTGTGATCTTATG 604

QY 575 CTAGGCGAGTATAGCCGAGGAGTATGGTGTTCAGCGCGTGTAAACAATTCGCTGGC 634

Db 605 CCAAGCTATAGTAAGCAGAGGAGATATGTTATAGGCCAGAGATGATTTGTTGGC 664

QY 635 CTCAGATGGCTGGCAGTATCCCTCTTCCATATAGACAGCTTTGATTTGGAGCGACCTAC 694

Db 665 CCCCAGTGGCTGGCATGGTACCTTCTGCTTCTGATCATGTTTGTGGAAGGAGATCTAC 724

QY 695 CTCATAGATATCCTCAAAAGGACCTGGTAAATATATAGATGCATTTGGTGGATTCCAG 754

Db 725 CACTGAAGTTCCACAGAGAGATCTTGTAATCTAAGAAATGATGTTGCGGTTACTA 784

QY 755 AGCATGATCAAGCAATAGAACATCCGGTACTTTTCATTTGGAGCTGTGTGCAAGCTTG 814

Db 785 ATCATGAGTCGAGTGAACAAAATATCTCGTACTTACCTTGGTGTGTGAGAGAACTTG 844

QY 815 ACTATTGAAGAGGTTGGAGTTAATGTTATTAATTCCTCCCTGCATGAGTCAACG 874

Db 845 ATCACTTGAAGAGAACTTGGTGTCAACTGTATAGACTAATGCCCTGTCCAGAGTTCAATG 904

QY 875 AGCTGGAGTACTCAACCTCTTCTTC- - - - - CAAGATGAACCTTTTGGGAT 919

Db 905 AGCTGGAGTACTATAGTTATAACTCTGTATTGGCGACTACAAGTTTAACTTTTGGGCT 964

QY 920 ATTCTACCAATAAATCTTTTCAACAATGACAGATACATCAGCGGGGATAAAACT 979

Db 965 ATTCTACTGTCAATTTCTTTTCTCCAATGGGAAGATACCTCATCTGCTGCTTAAGTAAT 1024

QY 980 GTGGCGGTGATGCCAATAAATGAGTTCAAACTTTTGAAGAGAGGCTCACAAACGGGAA 1039

Db 1025 GCGGCTCGGTGCAATAAACGAATTTAAGTATCTTGTCAAGGAGACATAAACGTGAA 1084

QY 1040 TTGAGGTGATCTGATCTTCTTCAACCATACAGCTGAGGGTAATGAGTAATGGTCCAA 1099

Db 1099

Db 1085 TCGAGGTTATCATGGATGTGTTTCAATCACACTGCTGAAGGAATGAATAATGGTCCCA 1144  
Qy 1100 TATTATCAATTAAGGGGTGCAATAACTATACATATATATCTTGACACCAAGGAGAGT 1159  
Db 1145 TACTATCATTTAGAGGCAATTGACAAACAGTGTGTTTATACGCTAGCTCTTAAGGTTGAAT 1204  
Qy 1160 TTTATTAATCTTCTGGCTGTGGGATACCTTCACTGTAATCATCTGTGTGTTCTGTCAT 1219  
Db 1205 TTTTCACTACTCAGGATGTGGAAATACCTTCACTGTAATCATCTGTAATCATCTGTCAT 1264  
Qy 1220 TCATTTAGATTTGTTTAAAGTACTGGGTGACGGAATGCAATGTGTGTTGTTTCTGTTTG 1279  
Db 1265 TTTATAGTGGATTTGCTTGAGATATTGGGTACCAGAAATGCACGTAGATGGCTTCCGCTTG 1324  
Qy 1280 ATCTTCATCCATTAATCACAGAGGTTCCAGTCTGTGGATCCAGTTAAGCTGTATGGAG 1339  
Db 1325 ATCTTGCTTCTATCTTACAGAGTACAGTCTGTGGATGCTGTAAATGCTGTATGGAA 1384  
Qy 1340 CTCCAATAGAGGTGACATGATCACACACAGGACACCTCTTGTACTCCACCACTTATG 1399  
Db 1385 ATTCAATTGACGGTGAAGTATCACACACAGGACCTCTCTCACAGCCCACTTGTG 1444  
Qy 1400 ACATGATCAGCAATGACCAATCTTGGAGGCTCAAGCTCATGTGTGAAGCATGGGATG 1459  
Db 1445 ATATGATTAGCAATGATCCAAATCTTCTGGAGTAAAGCTTATAGCTGAAGCATGGGAT 1504  
Qy 1460 CAGGAGCCCTATCAAGTAGGTCAATTCCTCACTGGATGTTTGTCTGTAGTGAATG 1519  
Db 1505 GTGAGGCTTTTACCAAGTTGGCATGTTCCGCACTGGGTATCTGTGGATGGGAAG 1564  
Qy 1520 GGAAGTACCGGCAATGTGCGTCAATTCATTAAAGCACTGATGATTTGCTGTGGTT 1579  
Db 1565 GAAAGTACCGTGACATGGTACGGCAGTTTCATCAAGGCACTGATGGGTTTCTGCGGCT 1624  
Qy 1580 TTGCGGATGCTTTTGGAGTCCACCTATACAGGTAAGTTGTGGCAATCTGTGA 1639  
Db 1625 TTGCTGAATGCTTTTGGAGGCCAAATCTATACAGAAAGGAGGAAGAAACCATGGA 1684  
Qy 1640 AATGAGTTGATGAATGTCACCTGGATTTTATATATATACCATGATGATACATCTA 1699  
Db 1685 ACAGTATAATTTGCTGTGTCACCATGTTTACTTTGGCTGATTTAGTGACATACA 1744  
Qy 1700 AATATATAAATCATAGTGTATGATATG 1729  
Db 1745 ACRATAACCAATTTGGCAATGGAGAG 1774

RESULT 7  
ABZ12413

ID ABZ12413 standard; DNA; 2352 BP.

XX AC ABZ12413;

XX XX 21-JAN-2003 (first entry)

XX XX Arabidopsis thaliana stress regulated gene SEQ ID NO 219.

XX XX Arabidopsis thaliana.

XX XX Arabidopsis thaliana.

XX XX WO200216655-A2.

XX XX 28-FEB-2002.

XX XX 24-AUG-2001; 2001WO-US026685.

XX XX 24-AUG-2000; 2000US-0227866P.

XX XX 26-JAN-2001; 2001US-024647P.

XX XX 22-JUN-2001; 2001US-0300111P.

XX XX (SCRI ) SCRIPPS RES INST.

XX XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;  
XX WPI; 2002-304127/34.  
XX Identifying a stress condition to which a plant cell has been exposed and  
XX producing plants with increased tolerance to these abiotic stresses.  
XX Claim 144; SEQ ID NO 218; 577pp + Sequence Listing; English.  
XX The invention relates to identifying a stress condition to which a plant  
XX cell has been exposed, comprising: (a) contacting nucleic acid  
XX representative of expressed polynucleotides in the plant cell with an  
XX array or probes representative of the plant cell genome; and (b)  
XX detecting a profile of expressed polynucleotides in the plant cell  
XX characteristic of a stress response. The method is useful in the  
XX production of transgenic plants, cells and seeds and in producing plants  
XX with increased tolerance to abiotic stress. The present sequence is that  
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
XX in methods of the invention. Note: The sequence data for this patent is  
XX not represented in the printed specification but is based on sequence  
XX information supplied to Derwent by the European Patent Office

XX SQ Sequence 2352 BP; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;

Query Match 22.0%; Score 658.4; DB 6; Length 2352;

Best Local Similarity 71.2%; Pred. No. 5e-132;

Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

Qy 389 TCCTCAGATAGGTTGACCGAGGAGTTCCCTTGACCCCTGATGATCGGACCGGA 448  
Db 323 TCCGTGAGCAAAAGTACCGGAGAGATTACGTTGATCCATCAAGGAATAGACTGCC 382  
Qy 449 AGCTGTGCATGCTCTTTCATCGAAGCGAGCTGCACCAATGTTTACGGGTACAGTTG 508  
Db 383 ATGTTTGGCATGTTCTTGAGAGAGATTTCAGAGATATGTTGATGTTATAGATTG 442  
Qy 509 ACGGCACCTTTGCTCCTCACTGCGGGCACTACCTTGATGTTTCCAAATGCTGCTGGATC 568  
Db 443 ATGGCAAGTTTCTCCTGAGAAGGTCTATTATGATTCTCTCAACATTTATTGGATC 502  
Qy 569 CTTATGCTAAGCAGTATAGCCAGGAGTATGGTTTCCAGCGCTGTAACAATT 628  
Db 503 CTTACGAAAGGCAATTATAGCAGAGATGAGTTTGGAGTTTGGGACTGATGATAAT 562  
Qy 629 GCTGCTCAGATGGCTGCGATGATCCCTCTTCCATATAGCAGCTTTTGAITGGGAAGCG 688  
Db 563 GTTGGCTCAATGCGGTGATGGTACCCTCGTGAGGAAGAGTTTCAITGGGAAGGG 622  
Qy 689 ACCTACCTCTAAGATATCCTCAAGGACCTGGTAAATATATGAGATGACATTCGCTGGAT 748  
Db 623 ATATGCATCTGAAGCTTCCACAGAAAGATCTTGTATATATGAAATGATGTCGAGGTT 682  
Qy 749 TCACGAAGCATGATTCAAGCAATGAGAACATCGGGTACTTTCATTGAGCTGTGTCGA 808  
Db 683 TTACAAGGCAATGCTTAGTAAATGAAATTTCCCTGGCACAATACAGGGTGTTCAGAGA 742  
Qy 809 AGCTTGACTATTGGAAGGAGCTTGGAGTTAATTTGTAATTAATGATCCCTGCCATGAGT 868  
Db 743 AGCTTGACCATTTGAAGGAGCTTGGGATAAATTTGATAGAATTAATGCAATGTCACGAGT 802  
Qy 869 TCAAGAGCTGGAGTACTCAACCTCTCTTC-----CAAGATGACTTTT 913  
Db 803 TTAATGAGCTGGAGTATTACAGCTACAATACGATTTTGGGAGACCCACAGGGTAAATTTT 862  
Qy 914 GGGGATATTTACCATAAACTTTCTTTTCCCAATGACAAGATACACATCAGCGGGGATAA 973  
Db 863 GGGGTTACTCTACCATTTGGTTCTTCTCGCCCATGATCAGATACGATCAGCAAGCTCTA 922  
Qy 974 AAAACTGTGGGCGTATGCCATAAATGAGTTCAAACTTTTGTAGAGAGGCTCAACAAC 1033  
Db 923 ACAATTTTGTGACGAGCCATAAATGAATCAAAATTTCTTTTAAAGAGGACACATAAAC 982

QY 1034 GGGGAATTGAGGTGATCTCTGATTTGTTCTTCAACATACAGCTGAGGGTAATGAGAATG 1093  
 XX |||||  
 PS |||||  
 Db 983 GAGGAATTGAGGTAATCATGATGCTGCTTTGAACACACAGCGGAAGGAATGAAAAG 1042  
 QY 1094 GTCCAAATATATCAATTTAAGGGGTGATATATCACTATATATGCTTGACCCCAAGG 1153  
 XX |||||  
 PS |||||  
 Db 1043 GGCCCAATTTCTCAATTTAGAGGAGTTGATAACAGTGTCTATTACATGCTTTGCTCCAAAGG 1102  
 QY 1154 GAGAGTTTATAACTATTCTGGCTGTGGGAATACCTTCAACTGTATATCATCTCTGGTTC 1213  
 XX |||||  
 PS |||||  
 Db 1103 GCGAGTCTATAATTAATTCAGGCTGTGGTAATCAATTCATCACTGCAATCATCTGTGGTGC 1162  
 QY 1214 GTCAATTCATTTAGATTTTAAAGTACTGGGTGACGGAATGCAATGTTGATGTTTTC 1273  
 XX |||||  
 PS |||||  
 Db 1163 GTCAATTCATATTGGATTGCTGAGATATTGGGTTACAGAAATGCAATTTGACGGCTTC 1222  
 QY 1274 GTTTTGATCTTGCATCATATGACAGAGTTCCAGTCTGTGGATCCAGTTAACTGT 1333  
 XX |||||  
 PS |||||  
 Db 1223 GCTTTGATCTTGTTCATCAATGTCAGGAGCAGCCCTTTGGATGAGCCCAATGTTT 1282  
 QY 1334 ATGAGCTCCCAATAGAAGGTGACATGATCAACAGGACACCTCTTGTCTTACTCCACAC 1393  
 XX |||||  
 PS |||||  
 Db 1283 ACGGGCTGATGTAGAAGGTGACTTGTCTCAACTGGTACTCTTATAGCTGCCCTCCAG 1342  
 QY 1394 TTATTGACATGATCAGCAATGACCAATCTTGGAGCGTCAAGCTCATTTGCTGAGCAT 1453  
 XX |||||  
 PS |||||  
 Db 1343 TAATTGACATGATAAGTAATGATCCAAATCTCCGCGGTGTTAAGCTAATAGCTGAAGCAT 1402  
 QY 1454 GGGATGAGGAGGCGCTCTATCAAGTAGGTCAATTTCCCTCACTGGAATGTTTGGTCTGAGT 1513  
 XX |||||  
 PS |||||  
 Db 1403 GGGATGCGGGTGGGCTGTACCAAGTTGGCATGTTCCACACTGGGTATTTGGTCTGAGT 1462  
 QY 1514 GGAATGGAGTAGTACCGGACATTTGTGCTCAATTCATTAAGGACGATGATGATTTGCTG 1573  
 XX |||||  
 PS |||||  
 Db 1463 GGAATGGAAGATTTCCGGGATGTTGTGAGACAGTTTCATAAAGGACCGGATGGCTTTCTG 1522  
 QY 1574 GTGGTTTGGCGAATGCTTTGTGGAGTCCACACTATACCAAGGTAAGTTG 1625  
 XX |||||  
 PS |||||  
 Db 1523 GTGCTTTTGTGATGCTCTGTGGAGCCCAATCTGTACCAAGGAGGTAG 1574

RESULT 8  
 ADA67900  
 ID ADA67900 standard; DNA; 2352 BP.

XX AC ADA67900;

XX XX 20-NOV-2003 (first entry)

XX DE Arabidopsis thaliana gene, SEQ ID 141.

XX KW Plant; bacterial infection; fungal infection; viral infection; ds.

XX OS Arabidopsis thaliana.

XX OS Arabidopsis thaliana.

XX PN WO2003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX XX Identifying at least one gene involved in plant resistance or response to

PT pathogenic infection for conferring resistance or tolerance to a plant to

PT gene expression.

PS Claim 6; SEQ ID NO 141; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.

XX Sequence 2352 BP; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;

Query Match 22.0%; Score 658.4; DB 7; Length 2352;

Best Local Similarity 71.2%; Pred. No. 5e-132;

Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

QY 389 TGCTGCAGATAGGTGACCGAGAGGTTCCCTTGACCCCTGATGAATCGGACCGGA 448

Db 323 TCCGTGAGAACAAAGTGACGGAGAGATTTCAGCTTGATCCATCAAGGAATAGAACTGCC 382

QY 449 ACGTGTGCAATGCTTTCATCGAAGCGGAGCTGCACACATGCTTTACGGGTACAGGTCG 508

Db 383 ATGTTGGCATGTGTTCTTGAGAGGAGATTTCAAAGATATGTTGTATGGTTATAGATTG 442

QY 509 ACGGCACCTTTGCTCTCCTGCGGCACTACCTTGATGTTTCCAAATGTCGTGTGGATC 568

Db 443 ATGCAAGTTTCTCTCGAAGAGGTCAATATATGATTCCTCCCAATTTATTTGATC 502

QY 569 CTTATGTAAGCGATGATAGCGAGGAGTAGTGTGTTCCAGCGGTGTTAAACAAAT 628

Db 503 CTTACGAAAGCAATTAATAGCAGAGATGAGTTTGGAGTTTGGGACCTGATGATAAAT 562

QY 629 GCTGSCCTCAGATGCTGGCATGATCCTCTTCCATATAGCACGTTTGTGTTGGAAGCG 688

Db 563 GTTGGCTCAAATGGCGTGTATGTTACCCACTGTGAGGAGAGTTTGTGTTGGAAGGG 622

QY 689 ACCTACCTCTAAGATATCTCTCAAAGGACCTGTAATATATGATGATGATGATGATGAT 748

Db 623 ATATGATCTGAAGCTTCCACAGAAAGATCTTGTATATATGAAATGATGATGATGATGAT 682

QY 749 TCACGAGCATGATCAAGCAATGTAACATCCGGGTACTTTTCATTTGGAGCTGTGTCGA 808

Db 683 TTACAGGCGATGATGATGATAAATTTGAATTCCTGCGCACATACAGGGTGTTCAGAGA 742

QY 809 AGCTTGACTATTGAAGAGGCTTGGAGTTAATTTGATTTGAATTAATGCCCTGCCATGAT 868

Db 743 AGCTTGACCAATTTGAGGAGCTTGGGATAAATTTGATAGAATTAATGCCATGTCAACGAT 802

QY 869 TCAAGAGCTGAGTACTCAACCTCTCTTC-----CAAGATGNACTTTT 913

Db 803 TTAATGAGCTGGAGTATTACAGCTACAATACGATTTTGGGAGACCAACAGGGTAAATTTT 862

QY 914 GGGATATTCTACCAATAAATTTCTTTTCCCAATGACAGATACACATCAGGCGGGATAA 973

Db 863 GGGGTACTCTACCAATTTGGGTCTTCTGCGCCATGATCAGATGCGCATCAGAGCTCTA 922

QY 974 AAAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTGAAGAGAGGCTCACAAC 1033

Db 923 ACAATTTTGTGGAGCGAGCCATAAATGAATTTCAAAATTTCTTTGAAGAGGACATTAAC 982

QY 1034 GGGGAATTTGAGTGTATCTGATGCTGTCTTCAACCATACAGCTGAGGGTAATCAGAAATG 1093

Db 983 GAGGAATTTGAGTAAATCATGATGCTCTTTGAACACACAGCGAAGGAATGAAGAAG 1042

QY 1094 GTCCAAATTTATCAATTTAAGGGGTGCAATAACTACTACTACTATGCTTTGACCCCAAG 1153

Db 1043 GGCCCAATTTCTCATTTAGAGGAGTTGATAACAGTGTCTATTACATGCTTGTCTCCAAAG 1102





Db 1268 GTGAATTTTCAACTACTCAGGATGTGGAATACCTTCAACTGTATAATCCCAATTGTAC 1327  
 Qy 1214 GTCAATTCATTTAGATTTTAAAGATACCTGGGTGACGGAATATGCTATTTGATGGTTTTTC 1273  
 Db 1328 GTCAAT---TTATAGTATGCTGAGATATTGGTTACCGAATGCGATACATGGCTTC 1384  
 Qy 1274 GTTTTGTATCTGCATATCAATGACAGAGTTCAGTCTGTGGATCCAGTTAAGCTGT 1333  
 Db 1385 GCTTTGTATCTTCTTCTATCTTACAAAGAAAGTAGCAGCTCTGTGGAATGCTGTAATGTCT 1444  
 Qy 1334 ATGAGCTCCCAATAGAGGTGACATGATCAACAGGAGCACCTCTTTGTTACTCCACCAC 1393  
 Db 1445 ATGGAATTCNAITGACGGTGACGTGATCACAGGACCTCTCTCAAGGCCACCAT 1504  
 Qy 1394 TTATTGATGATCAGCAATGACCCCAATTTCTGAGGCGTCAAGCTCATTTGCTGAAGCAT 1453  
 Db 1505 TGATTGATATGATTAGCAATGATCCAACTCTCTGAGTAAAGCTTATAGCTGAAGCAT 1564  
 Qy 1454 GGGATGACGAGGCGCTCTATCAAGTAGTCAATTCCTCACTGGAATGTTTGTCTGAGT 1513  
 Db 1565 GGGATTGTGAGGCGCTTTACCAAGTTGGCATGTTTCCGCACTGGGTATCTGTGCGAGT 1624  
 Qy 1514 GGAATGGGAAGTACCGGACATTTGCGTCAATTCATTAAGGCGTCAAGCTGATGGAATTTGCTG 1573  
 Db 1625 GGAACGGAAAGTACCGTGACATGCTACGGCAGTTTCATCAAGGCACCTGATGGGTTTCTG 1684  
 Qy 1574 GTGGTTTTCGGAATGCTTTGGAAGTCCACACCTATACAGGTAAGTTGTGGCAATA 1633  
 Db 1685 GGGCTTTTGTGGAATGCTTTGGAAGCCCAATCTATACCAAGAGGAGGAAGAAAC 1744  
 Qy 1634 CTCTGAATGAGTTGAGTGAATGTCACCTCGATTTTATATATATACCATGATGATACA 1693  
 Db 1745 CATGGAACAGTATAAATTTCTGTGTGTCGCCACAGTGTTTTACTTTGGCTGATTTAGTGA 1804  
 Qy 1694 CATCTAATATATAACAATCATAGTGTATGATG 1729  
 Db 1805 CATACAACATAAACACAAATTTGGCAATGGAGAGG 1840

## RESULT 10

AAT96754  
 ID AAT96754 standard; cDNA to mRNA; 2133 BP.

AC AAT96754;

DT 25-MAR-2003 (revised)  
 DT 08-MAY-1998 (first entry)

XX S. tuberosum debranching enzyme cDNA.

XX Debranching enzyme; PDB; potato; transgenic plant; starch; industry;  
 XX food manufacture; ss.

OS Solanum tuberosum.

XX Key Location/Qualifiers  
 FH 1. 1822  
 CDS /\*tag= a  
 FT /product= "debranching enzyme"  
 FT /note= "partial coding sequence"

XX DE19618125-A1.

XX 13-NOV-1997.

XX 06-MAY-1996; 96DE-01018125.

XX 06-MAY-1996; 96DE-01018125.

XX (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.

XX WPI; 1997-551167/51.

DR P-PSDB; AAW36602.  
 XX DNA encoding potato debranching enzyme - useful for producing recombinant  
 PT enzyme or transgenic plants for use in food production or in industry.  
 XX Claim 1; Page 14-17; 20pp; German.  
 XX This cDNA sequence encodes a novel potato debranching enzyme (PDE). This  
 CC gene can be used in the production of transgenic plants especially starch  
 CC storing plants e.g. Cereal or potato plants. Other nucleic acid molecules  
 CC could be designed which specifically hybridise to the PDE transcript and  
 CC inhibit its translation. Vectors containing this gene can be linked in  
 CC sense orientation with regulatory elements that ensure its transcription  
 CC and translation in prokaryotic and eukaryotic cells. The starch produced  
 CC from such transgenic plants could be used in the manufacture of foods or  
 XX industrial products. (Updated on 25-MAR-2003 to correct PA field.)  
 XX Sequence 2133 BP; 650 A; 392 C; 475 G; 616 T; 0 U; 0 Other;

Query Match 19.2%; Score 575.4; DB 2; Length 2133;

Best Local Similarity 59.8%; Pred. No. 4.1e-114;

Matches 799; Conservative 0; Mismatches 331; Indels 15; Gaps 1;

Qy 600 GTATGTTTCCAGCGGTGTAAATTCGTGCTCAGATGCTGGCATGATCCCTCT 659  
 Db 1 GAAATTCGSCACGAGGCGCAGAGGATGATTGTTGGCCCCCAATGGCAGCGCATGGTACCTTC 60  
 Qy 660 TCCATATAGCACGTTTGAATGGGAGGCGACCTACCTTAAGATATCTCAAAAGGACCT 719  
 Db 61 TGCCTCTCATCAGTTTGAATGGGAGGAGAGATCTATTACTGAAGTTTCCACAGAGATCT 120  
 Qy 720 GGTAAATATATGAGATGCACTTGCCTGGATTCCAAAGCATGATTCAAGCAATGTAGAACA 779  
 Db 121 TGTAACTATGAATGCATGTCCTGGATTTCACAAATCATGAGTCGAGTGAACAAAATA 180  
 Qy 780 TCCGGTACTTTCAATGGAGCTGTGCGAGCTTGCTGAGCTTATTTGAGAGCTTGGAGTTAA 839  
 Db 181 TCCCTGGTACTTACCTTGGTGTGTGGAGAAACCTTGATCCTTGGAAGAACTTGGTGTCAA 240  
 Qy 840 TTGTATTGAATTAATGCTCCCATGAGTTCAACAGCTGGAGTACTCAACCTCTTCTTC 899  
 Db 241 CTGTATAGAGCTAATGCTCTGACGAGTTCAATGAGCTGGAGTACTATAGTTATACCTC 300  
 Qy 900 -----CAAGATGAACCTTTTGGGGATTTCTACCAATAAATCTTTTTCACC 944  
 Db 301 TGTATTGGGCGACTACAAGTTTAACTTTTGGGGCTATTCTACTGTCAATTTCTTTTCTCC 360  
 Qy 945 AATGACAGATACACATCAGCGGGGATAAATAAAGCTGTGGGCGTGATGCCATAATGAGTT 1004  
 Db 361 AATGGGAAGTACTCGTCTGCTGTCTAAGTAAATGCGGCTCGTGCGAATAAAGCAATT 420  
 Qy 1005 CAAACCTTTTGTAAAGAGAGGCTCACAAACGGGGAAATTTGAGTGATCTCTGGATGTGCTT 1064  
 Db 421 TAAGTATCTTGTCAAGGAAGCACATAAACGTGGAATCGAGGTTATCATGAGTGTGTTT 480  
 Qy 1065 CAACCATACAGCTGAGGTAATGAGATGTGCTCAATATATCATTTTAAGGGGTGCTATAA 1124  
 Db 481 CAATCACACTCTGCTGAAGGAAATGAAATGGTCCCATATCATATTAGAGGCATTTGACAA 540  
 Qy 1125 TACTACATATATATGCTTGCAACCAAGGAGAGTTTTATAAATTTCTTGGCTGTGGGAA 1184  
 Db 541 CAGTGTGTTTATACGCTAGCTCTTAAGGGTGAATTTTACAACTACTCAGGATGTGGAAA 600  
 Qy 1185 TACCTTCAACTGTAAATCATCTGTGGTTCGTCAATTCATTGTAGATTGTTTAAAGTACTG 1244  
 Db 601 TACCTTCAACTGTAAATCAATCCATTGACGTCAATTTTATAGTGGATTGCTTGAATATTG 660  
 Qy 1245 GGTGACGGAATGATGTTGATGTTTGTGTTTGTGCTTGTGATCTTGCATCCATAATGACAGAG 1304  
 Db 661 GGTACCGAATGACGTAGATGGCTTCCGCTTGTGATCTTGTCTTCTATCCTTACAAGAG 720  
 Qy 1305 TTCCAGTCTGTGGGATCCAGTTAAGTGTATGAGAGTCCCAATAGAAGGTGACATGATCAC 1364

Db 721 TAGCAGCTCGTGGAAATGCTGTAATGCTCTATGGAAATTCAAATTGACGGTGACATGATCAC 780  
 QY 1365 AACAGGACACCTCTTCTTACTCCACCACCTATTGACATGATCAGCAATGACCAATTCT 1424  
 Db 781 CACAGGCACCTCTCTCAAGCCACCATTTGATGATGATGATGATGATGATGATGATGAT 840  
 QY 1425 TGGAGGCGTCAAGCTCAATGCTGAAGCATGGGATGAGGAGGCTCTATCAAGTAGGTCA 1484  
 Db 841 TAGTGGAGTAAAGCTTATAGCTGAAGCATGGGATTTGTGGAGGCTTTTACCAAGTTGGCAT 900  
 QY 1485 ATTCCCTCACTGGAAATGTTGGTCTGAGTGGAAATGGGAAGTACCGGACATTTGGGTCA 1544  
 Db 901 GTTTCGCACTGGGATGCTGGTGGAGTGGAAAGTACCGGAAGTACCGTACATGATGATGATCA 960  
 QY 1545 ATTCATTAAAGGCACTGATGATTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1604  
 Db 961 GTTCATCAAGGCACTGATGGTCTTCTGGGCTTTTGTGAATGCTTTTGTGAAGGCC 1020  
 QY 1605 ACACCTATACCAAGTATGTTGTCATATCTTGAATGATGATGATGATGATGATGATGATG 1664  
 Db 1021 AAATCTATACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
 QY 1665 ATTTTATATATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1724  
 Db 1081 CGATGTTTACTTTGGCTGATTTAGTGACATACACAAATAACAAATTTGGCAATGG 1140  
 QY 1725 ATATG 1729  
 Db 1141 AGAGG 1145

## RESULT 11

AAX34655  
 ID AAX34655 standard; DNA; 9289 BP.

XX AAX34655;

DT 17-OCT-2003 (revised)

DT 05-JUL-1999 (first entry)

XX Hexaploid wheat DBE genomic sequence.

XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;  
 KW starch branching enzyme; starch soluble synthase; debranching enzyme;  
 KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;  
 KW grain softness protein 1; bacterial isomylase; glycogen synthase;  
 KW WSBE 1-D4 gene; ss.

XX Aegilops tauschii.

XX Key Location/Qualifiers

FT CDS 1..9287

FT /\*tag= a

FT /note= "the start codon is not indicated; contains 146  
 internal stop codons"

XX WO9914314-A1.

XX 25-MAR-1999.

XX 11-SEP-1998; 98WO-AU0000743.

XX 12-SEP-1997; 97AU-00009108.

XX 20-MAR-1998; 98AU-00002509.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX (AUSU ) UNIV AUSTRALIAN NAT.

XX (GOOD-) GOODMAN FIELDER LTD.

XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Li Z, Morell M, Rahman S;

XX WPI; 1999-229525/19.

DR P-PSDB; AAY06919.

XX New isolated cereal plant enzyme genes used for, e.g. expression of  
 PT antisense sequences of granule bound synthase.

XX Claim 14; Page 103-115; 171pp; English.

XX The invention relates to a novel enzyme of starch biosynthetic pathway in  
 CC a cereal plant, where the enzyme is selected from starch branching enzyme  
 CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme  
 CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of  
 CC rice or maize. The methods and products can be used for targeting  
 CC expression specifically to the endosperm of the seeds of cereal plants  
 CC such as wheat or barley. They can be used for the expression of e.g.  
 CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.  
 CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial  
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be  
 CC used for modifying the characteristics of starch produced by a plant. The  
 CC present sequence represents the wheat DBE genomic DNA sequence. (Updated  
 CC on 17-OCT-2003 to standardise OS field)

XX Sequence 9289 BP; 2477 A; 1909 C; 2040 G; 2863 T; 0 U; 0 Other;

Query Match 17.8%; Score 533.4; DB 2; Length 9289;

Best Local Similarity 95.1%; Pred. No. 7.9e-105;

Matches 562; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 GGTCTGGGGCCGCGCGCGCTGCGACCGTGGCGAGCCCAATCCGACGCGGGGAGGGGG 60

Db 1943 GCGCGGGCGCGCGCGCGCTGCGACCGTGGCGAGCCCAATCCGACGCGGGGAGGGGG 2002

QY 61 TCGGGGAGGTGTGCGCGCGGTGTGCGAGCGCGCGACCAAGGTAGAGACAG--GGGG 117

Db 2003 TCGGCGAGGTGTGCGCGCGGTGTGCGAGCGCGCGACCAAGGTAGAGACAGCG 2062

QY 118 AGGAGACGAGCCGCTGCGCGAGGACAGGTACGCGCTCGCGCGCGCGTGCAGGGTCTCG 177

Db 2063 ACGAGGAGGCGGTGCGCGAGGACAGGTACGCGCTCGCGCGCGCGTGCAGGGTCTCG 2122

QY 178 CCGGATGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 237

Db 2123 CCGGAATGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 2182

QY 238 ATTCCGCGGAGCCACCGCGCGCGCGCTGCGCTCTTACGCCAGAGATCTCAAGCGG 297

Db 2183 ACTCCGCTGAGCCACCGCGCGCGCTGCGCTCTTACGCCAGAGATCTCAAGCGG 2242

QY 298 TGGGGTTGCTCCCGAGTAGATTTCATCAGCTTCGCTGCGCGCGCGCGCGCGCGCGCG 357

Db 2243 TGGGGTTGCTCCCGAGTAGATTTCATCAGCTTCGCTGCGCGCGCGCGCGCGCGCG 2302

QY 358 GCCTGCAATTTAAGTTTGTACTGGGGCAATGCTGCAGGATAGGTGACCGAGGAGTT 417

Db 2303 GCCTGCAATTTAAGTTTGTACTGGGGCAATGCTGCAGGATAGGTGACCGAGGAGTT 2362

QY 418 CCGCTTGACCCCTGATGAATCGGACCGGAAACGTTGTCATGTCATGTCATGTCATGTCAT 477

Db 2363 TCCCTTGACCCCTGATGAATCGGACCGGAAACGTTGTCATGTCATGTCATGTCATGTCAT 2422

QY 478 CTGCACAAATGCTTTACGGGTACAGGTTCGACGCGCACCTTTGCTCCTCAGTCGCGGCAC 537

Db 2423 CTGCACAAATGCTTTACGGGTACAGGTTCGACGCGCACCTTTGCTCCTCAGTCGCGGCAC 2482

QY 538 TACCTTGATGTTTCCAAATGCTGTTGGTGGATCCCTTATGCTTAAGCGCAGTGATA 588

Db 2483 TACCTTGATGTTTCCAAATGCTGTTGGTGGATCCCTTATGCTTAAGCGCAGTGATA 2533

RESULT 12

ADCO8661

ID ADC08661 standard; DNA; 603 BP.

XX ADC08661;

AC



Matches 555; Conservative 0; Mismatches 227; Indels 3; Gaps 1;			
QY	2140	ATCAGGAGGAGGAAGAAACCTTGGCACAGTATCAACTTTGTATGTGCACATGATGGAT	2199
DB	577	ACCAGAAAGGAGGAGAAACACCTGGACACAGTATAAATTCGTGTGTGCCACGATGGTT	636
QY	2200	TTACACTGGCTGATTTGGTAAACATATAATTAAGAAAGTACAAATTTACCAATGGGGAGAAC	2259
DB	637	TTACTTTGGCTGATTTAGTGACATACACAAATAAACAATTTGGCAATGGAGAGGACA	696
QY	2260	ACAGAGATGAGAGAAATCAATCTTAGCTGGAAATGTGGGAGGAGGAGAAATTCGCAA	2319
DB	697	ACAAGAGCGGGAGAAATCAAAATTAATTTGGAATTTGGTGAAGAGGAAATTTGCAA	756
QY	2320	GATTGTCTGTCAAAGATTGAGGAGGAGGAGATGCGCAATTTCTTTGTCTCATGG	2379
DB	757	CTATCTTTATCAAGAAATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	816
QY	2380	TTTCTCAGAGGTTTCCATGTTCTACATGTTGATGATGATGATGATGATGATGATGATG	2439
DB	817	TTTCCCAGGTTTCCCATGATATATATGCGGATGATGATGATGATGATGATGATGATG	876
QY	2440	ACAAACAATACATCTGCGCATGATTTCTTATGTCAATTTTTCGCTGGGATATAAAGAAC	2499
DB	877	ACAACAACAGTATTTGCGCATGATATATATTAATTTACTTCCGTTGGGATAGAAGATG	936
QY	2500	AA----TACTCTGAGTTGACCGATTCGTGCTCATGACCAATTCGCAAGAGTGCG	2556
DB	937	AATCTTCTGATTTTGTGAGATTTTGGCGCTCATGACCAATTCGCGCATGAATGTG	996
QY	2557	AGGCTCTTGGCTTGAGACTTTTCCACGGCCAAACGGCTGCAATGCGATGTCATCAGC	2616
DB	997	AATCACTGGGATTAGATGGTTTCTTACAGCAGAAAGCTGCAATGSCATGGTCACTC	1056
QY	2617	CTGGAGGCTGATGTTGCTGAGAAATAGCCGATTCGTGCTTTCATGAAAGATGAAA	2676
DB	1057	CTAGAACTCCAGATTTGTTCTGAAACAAGTCAATTCGTGCTTTCATGAAAGATGAAA	1116
QY	2677	GACAGGGGAGATCTATGTCGCTTCAACACCGCACTTACCGCGCTTGTGAGCTCC	2736
DB	1117	TGAAGGAGAACTATATATGCTTTTAAAGCCAGCCATTTGCTGTAAAGATTAATTC	1176
QY	2737	CAGAGCGCGAGGCGCGGTGGGACCGGTGGTGGACAGAGGCAAGCCACCACTACG	2796
DB	1177	CAGATAGGCTGGTTATAGATGGCAGCGCTTTGTGGACAGAGGCAAGCCACCACTACG	1236
QY	2797	ACTTCTCAGCAGACATTAATCTGATGCGCTCTCACCATACACAGCTTCTCGCATTTCC	2856
DB	1237	ACTTCTTACAGACAGCTTCTCAGATGCTCAGTATTCATCATATTTCTTTTACTATCATCTG	1296
QY	2857	TCTACTCAACCTCTACCCCATGCTCAGCTACTCATCGGTCTATCTAGTATTTGGCCCTG	2916
DB	1297	TGGAGCGGACCACTATCCGATGCTCAGTATTCATCATATTTCTTTTACTATCATCTG	1356
QY	2917	ATGTT 2921	
DB	1357	CTGAT 1361	

RESULT 14

ID	ADC07811
XX	ADC07811 standard; DNA; 432 BP.
AC	ADC07811;
XX	18-DEC-2003 (first entry)
DT	Rice DNA sequence Seq ID77 related to grain filling.
DE	plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW	carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW	tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW	wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;

KW	gene; ds; plant.
XX	Oryza sativa.
XX	WO2003000905-A2.
XX	03-JAN-2003.
PD	21-JUN-2002; 2002WO-IB002450.
XX	22-JUN-2001; 2001US-0300112P.
PR	26-SEP-2001; 2001US-0325277P.
PR	20-DEC-2001; 2001US-0342327P.
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.
PA	Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
XX	Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
PI	WPI: 2003-229341/22.
XX	P-PSDB; ADC07812.
DR	New plant genes encoding polypeptides having an activity involved in or
PT	associated with the synthesis, metabolism or degradation of carbohydrates
PT	in the plant grain useful in generating plants having improved
PT	nutritional properties.
XX	Claim 2; SEQ ID NO 77; 130pp; English.
XX	This invention, in the area of plant biotechnology, relates to novel
CC	polynucleotides comprising a nucleotide sequence encoding a protein which
CC	is involved in or associated with the synthesis, metabolism or
CC	degradation of carbohydrates in the plant grain and the expression of
CC	which is up-regulated during grain filling. The plant is selected from
CC	corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC	sugarbeet, wheat, and rice. The invention may be useful for the
CC	improvement of protein, oil, starch, fibre and moisture content of the
CC	cereal grains. In addition, carbohydrate levels may be modified to a more
CC	desirable level using the present invention. The present sequence is a
CC	DNA sequence encoding a rice protein of the invention. Note: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/publishedpct_sequences.
XX	Sequence 432 BP; 89 A; 135 C; 104 G; 104 T; 0 U; 0 Other;

Query Match	9.2%; Score 275; DB 9; Length 432;
Best Local Similarity	82.8%; Pred No. 1.8e-49;
Matches 314; Conservative 0; Mismatches 65; Indels 0; Gaps 0;	

QY	2546	CAAGAGTCCGAGGCTTTGGCTTGAGGACTTTCACAGGCAACCGCTGCAGTGGCA	2605
DB	54	CAGACAATCGAGTCCCTTGGCTCGCAGACTTCCCAACAGCTCAACGGTTGCAITGGCA	113
QY	2606	TGGTCATCAGCTGGGAAGCCTGATTGGTCTGAGATAGCGATTGTTCCCTTTTCCAT	2665
DB	114	TGGCCATCAGCTGGGAACCTTGACTGGTCTGAGCAAGCCGTTTGTGGCTTCTCCAC	173
QY	2666	GAAAGATGAAAGACAGGCGAGATCTATGTGGCTTCAACACAGCACTTACCGCCGTT	2725
DB	174	GAAAGATGAAAGAGGCGAGATCTACGTGGCTTCAACAGCAGCACTTTCGCGCGGT	233
QY	2726	TGTTGAGTCCAGAGCGCGAGGCGCGGTGGGACCGGTGGTGGACAGAGGCAAGCC	2785
DB	234	TGTTGAGTCCAGAGCGCGAGGCTACCGCTGGGAGCGCGGTGGTGGACAGAGGCAAGCC	293
QY	2786	AGCACCATACGACTTCTCACCAGCACTTACCTGATCGGCTCTCACCATACACAGTT	2845
DB	294	AGGCTTATGACTTCTCACCAGCACTTACCTGATCGTGTGCTCAGCGCTCCACTGTT	353
QY	2846	CTCGATTTCTCTACTCCAACTCTACCCATGCTCAGTACTCATCGGTATCTCTAGT	2905
DB	354	CTCTCTTTCTCAACTCCAATCTTACGCCATGCTCAGTACTCTCTCTCTATCATCTTGA	413





QY	379	CTGGGCGAAATCTCTGCAGGATAGGGTGCACGAGGAGGTTCCTCTTGACCCCTCTGATGAAT	438
DB	450	-----GGATAGGGTGACCGAGGAGGTGCCCTCGATCCCTGCTCAAC	492
QY	439	CGGACCGGAACGTGTGSCATGTCCTTCATCAAGG---CGAGCTGCACAAATGCTGTAC	495
DB	493	CGAACGGGAAACGTGTGGCACTGTTCATCCACGGGACCGAGCTGCAGCGCATGCTCTAC	552
QY	496	GGGTACAGTTTCGACGGCACCTTTGCTCCTCACTCGGGCACTACCTTGATGTGTTTCCAAT	555
DB	553	GGATACAGTTTCGATGGCGTGTTCGCCCTCGAGCGCGGACGACTACGATGTGTCCAC	612
QY	556	GTCTGTGTGGATCCTTATGCTTAAGGCAGTGATTAAGCCGAGGGGAGTATGTTGTTCCAGCG	615
DB	613	GTGTGTGTGGATCCATACGCTTAAGCAGTGTGTAAAGCCGAGGTGAATATGTTGTGCTCGC	672
QY	616	CGTGTATAAATGTCTGSCCTCAGATGCTGGCATGATCCCTCTTCATATATAGCAGTTT	675
DB	673	CCTGGTGGTAGTTGTGTGGCTCAAAATGGCTGGTAGTCCCTCTTCCCTATATAAGTTT	732
QY	676	GATTGGGAAGCGACCTTACCTCTTAAGATATCCTCAAAAGGACCTGGTAATATATAGATG	735
DB	733	GATTGGCAAGGTGACCTACCCCTTTGGGTACCATCAGAAGGACCTTGTCATATATGAATG	792
QY	736	CACTTGCGTGATTCAGAAGCATTGTTCAAGCAATGTAGAACATCCGGGTACTTTCATT	795
DB	793	CATTGCGTGATTCACAAAGCAAACTCAAGCAAGCAAAACACCCAGGAACCTTACATT	852
QY	796	GGAGCTGTCTCGAAGCTTGACTATTTCAAGGAGCTTGCGAGTTAATTTGTTATGAATTAATG	855
DB	853	GGTGTGTCTCAAAGCTTGACCTCTAAAGGAACTTCGAGTGAACTGTATAGACTAATG	912
QY	856	CCCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTTCTTCCAAGATGAACCTTTGG	915
DB	913	CCCTGCCATGAGTTCAATGAGCTAGAGTACTTCAGCTCCTCTTCGAAGATGAACCTCTCG	972
QY	916	GGATATTCACATAAACTCTTTTACCAATGACAAGATACATCAGGGCGGATAAAA	975
DB	973	GGATATCCACAATAATTTTCTCACCAATGGCAAGATATCTTCAAGTGGCATAGA	1032
QY	976	AACGTGGCGGTGATGCCATAAATGAGTTCAAAACCTTTGTAAGAGAGGCTCACAAACGG	1035
DB	1033	GACTCTGGATGTGGTGCATAAATGAATTTAAAGCTTTGTAAGGAGGCGCCACAAAACGG	1092
QY	1036	GGAAATGAGGTGATCTCGATGTTGCTTCAACCATCAGCTGAGGGTAATGAGAAATGGT	1095
DB	1093	GGAAATGAGGTGATCATGGATGTTGTCCTTCAATCATCAGCTGAAGGTATATGAGAAAGGC	1152
QY	1096	CCAAATATTATCAATTAAAGGGGTGCATAATACATATATGCTTGCAACCAAGGGA	1155
DB	1153	CCAAATATTCTTTAGGGGATAGATAATAGTACATACTACATGCTTGACCTTAAGGGA	1212
QY	1156	GAGTTTATACATTTCTGGCTGTGGGATACCTTCACTGTATCATCTGTGGTTCGT	1215
DB	1213	GAGTTTATATAATTTCTGGTTGTGGAAATACCTTCAATTGTAATCATCTGTAGTCCGT	1272
QY	1216	CAATTCAATTGATGTTTAAAGATACCTGGGTGACGGAAATGCAATGTTGATGTTTTCGT	1275
DB	1273	GAAATTTATAGTGGATGCTTGGATACCTGGGTAAACAGAAATGCATGTTGATGGTTTCGT	1332
QY	1276	TTTGATCTTGATCCATTAATGACAGAGGTTCCAGCTGTGTGGATCAGTTTAACGCTGAT	1335
DB	1333	TTTGACCTTGATCTATCTACAGAGGATGCAAGTCTATGGGATCCAGTTAATGTGTAT	1392
QY	1336	GGAGCTCCAAATAGAAGGTGACATGATCAACACAGGGACACCTCTGTGTACTTCCACCACTT	1395
DB	1393	GGAGTCCAAATGGAAGGTGACATGATACGACAGGGACACCTCTTGTGTGCCCAACCTT	1452
QY	1396	ATTGACATGATCAGCAATGACCCAAATTTCTTGGAGGGGTCAAGCTCATTTGCTGAAGCATGG	1455
DB	1453	ATTGACATGATAGCAATGACCCAAATTTCTTGGAAATGTCAAGCTCATTTGCTGAAGCATGG	1512

Qy	1456	GATCGAGAGCCCTCTATCAAGTAGGTCAATCCCTCACTGGAAATGTTTGGTCTGAGTGG	1515
Db	1513	GATCGAGAGGTCCTCTATCAAGTTGGTCAGTTTCTCTCACTGGAAACGTTTGGTCAGAGTGG	1572
Qy	1516	AATCGGAAGTACCGGGACATTTGCGTCAATTCATTAAAGGCCACTGATGATTGCTGGT	1575
Db	1573	AATGGAAGTATCCGGATACCGTGGTCAGTTTCAACAAAGCACAAGATGATTTGCTGGT	1632
Qy	1576	GGTTTTCGCGAATGCTTTTGTGGAAATGCCACCTATACCAAGTAAAGTTGTGGCAATACT	1635
Db	1633	GCTTTTGTCTGAATGCCCTATGTGGAAATGCCACAGTTATAC	1671
Qy	1636	TGTAATGAGTTGAGTGAATGTCACCTGGATTTTTTATATATACCACATGATACACA	1695
Db	1672	-----	1671
Qy	1696	TCATAATATATAACAATCATAGTGTATGTCATATGCAATTTGGCTAAGAAATTTAGTGAT	1755
Db	1672	-----	1671
Qy	1756	ACACTAGTGCTATATATAGGTTTTAAACCCAACTTCCCAATGAAGGAACATAGGCGTTT	1815
Db	1672	-----	1671
Qy	1816	CTAGTTATCTTATTTATTTGTCGGTGAAATAATCACTGAAAAATTCAGCCCATGTCAAT	1875
Db	1672	-----	1671
Qy	1876	TTTTAGGGGGGAGAAACTATATTGATTTGCCCCCTTAAAGAAAGCCATCTCAGAAAT	1935
Db	1672	-----	1671
Qy	1936	TCATAGTAAGTTGCTTTTCTGTAAGAAAGGAAACGACTTCTCATCTTTCTATCGGTGC	1995
Db	1672	-----	1671
Qy	1996	TAACTTAGCTCGATGATATTTTGAAGATGAATGCCAAATTTAAATTTGTCGGATAATTG	2055
Db	1672	-----	1671
Qy	2056	ATCTGTTATTCAAAATTTCTATTTGGTTCTCTAGNAATCAACACGTAACCTTGTTAT	2115
Db	1672	-----	1671
Qy	2116	GGCACTGCAACTTCTTATTGATTAAATCAGGCAGAGGAGGAAACCTTGCCACAGATCA	2175
Db	1672	-----CAGCGGGGGGAGGAGCCCTTGSCACAGATCA	1705
Qy	2176	ACTTTGTATGTGCATGATGGAATTTACCTGGCTGAATTTGGTAAACATATATAGAAAT	2235
Db	1706	ACTTTGTATGTGCACACGATGGAATTTACCTGGCTGATTTGGTCACATACAATAGCAAGT	1765
Qy	2236	ACAAATTTCCAAATGGGGAGAAACAACAGAGATGGAGAAATCAAACTTTAGCTGGAAT	2295
Db	1766	ACAACTTGTCAATGTGTAGGACAACAGAGATGGGAAATCATATCTTAGCTGGAAT	1825
Qy	2296	GTGGGAGGAGGAATTCGGAAGATTTGCTGTCAAAAGATTTAGGAAGAGCGACATGC	2355
Db	1826	GTGGGAGGAGGAGAAATTTGCAAGTCTGTCACTCCGAGATTTAAGGAAGAGGCAAAATGC	1885
Qy	2356	GCAATTTCTTTGTTGTCTCATCTGTTTCTCAAGGATTCCAAATGTTCTACATGGGTGATG	2415
Db	1886	GCAATTTCTTTGTTGTCTTATCGTTTCTCAGGAGTTCCAAATGTTCTACATGGGCGATG	1945
Qy	2416	AATATGCCACACAAAGGGGGCAACAATACATCTGCCATGATTTCTTATGTCAAT	2475
Db	1946	AATATGTCACACAAAGGGAGGGAACAACAATACGTACTGCCCATGACCATTAATGTCAACT	2005
Qy	2476	ATTTTTCGCTGGGATAAAA-----AAGAACATACTCTGAGTTGACCCGATCTCTGCGCTCA	2532
Db	2006	ATTTTCGCTGGGATAAGAGGAAGAACATCTCTGATTTGTACAGATTTCTGCGCTCTCA	2065
Qy	2533	TGACCAAAATTTCCGCAAGAGGTGCGAGGGTCTTTGGCCTTTGAGGACTTTTCCAAACGGCCAAAC	2592



Db 2066 TGACCAATCCGCAAGAAATGTAATCTCTTGGCCCTTGAGGACTTCCCGACTTCAGAAC 2125  
Qy 2593 GCGTCAGTGGCATGTCATCAGCCTCGGGAAGCCTGATTGGTCTGAGAAATAGCCGATTTCG 2652  
Db 2126 GATTGAATGCGACGGTCAATCAGCCCGGAAGCCTGACTGCTCAGAGCCAGCCGATTTCG 2185  
Qy 2653 TTGCTTTTCATGAAAGATGAAGACAGCGCGAGATCTATGTGGCCTTCAACACAGCC 2712  
Db 2186 TTGCTTTTCATGAAAGATGAAGACAGCGCGAGATCTATGTGGCCTTCAACACAGCC 2245  
Qy 2713 ACTTACCGCGCTTGTGAGCTCCAGAGCGCGCAGCGCCGCTGGGAACCGGTGGTGG 2772  
Db 2246 ACCTTCGGGTGTTGTCGGCTTCCAGAGCGCTCTGGGTTCCGATGGAGCCCGTGGTG 2305  
Qy 2773 ACAGCGAAGCCAGCAGCAGATGCTTCTCCTACCGACGACTTACTCTGATGCGCTCTCA 2832  
Db 2306 ACAGCGAAGCCAGCAGCAGATGCTTCTCCTACCGACGACTTACTCTGATGCGCTCTCA 2365  
Qy 2833 CCATACACGCTTCTCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2892  
Db 2366 CCGCTTACCGCTTCT 2425  
Qy 2893 CGGTATCTCTAGTATTCGCGCTCTGATGTTTGAGAGACCAATATATA 2938  
Db 2426 CCATCATCTTGTATTCGCGCCCTGATGCTGGAAGAGCGGATACA 2471

RESULT 2

US-08-410-784A-1  
; Sequence 1, Application US/08410784A  
; Patent No. 5912413  
; GENERAL INFORMATION:  
; APPLICANT: MYERS, ALAN M.  
; APPLICANT: JAMES, MARTHA G.  
; TITLE OF INVENTION: ISOLATION OF SUI, A STARCH DEBRANCHING  
; TITLE OF INVENTION: ENZYME, THE PRODUCT OF THE MAIZE GENE  
; TITLE OF INVENTION: SUGARY 1  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes LLP  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/410,784A  
; FILING DATE: 24-MAR-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heine, Ph.D., Holliday C  
; REGISTRATION NUMBER: 34,346  
; REFERENCE/DOCKET NUMBER: ISU-002XX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-2290  
; TELEFAX: 617-451-0313  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2712 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...2454  
; OTHER INFORMATION:  
US-08-410-784A-1  
  
Query Match 33.4%; Score 1000; DB 2; Length 2712;  
Best Local Similarity 65.7%; Pred. No. 2.4e-226;  
Matches 1883; Conservative 0; Mismatches 350; Indels 633; Gaps 4;  
  
Qy 79 CGGTTGTCAGCGCGCGAGAGGTAGAGGAGAGGGGAGAGGAGCGCGGCTGG 138  
Db 233 CGGTGGCGCGAGCGGTGCGAGCGGAGAGGAGCGAGCGAGCGAGCGGCTGG 292  
Qy 139 AGGACAGGTGACGCGCTCGCGCGCGGTGCTCGCGGAAATCGCGCGCGCTGG 198  
Db 293 AGGAGAGGTTCCGCTGGCGCGCGGTGCTCGCGGAAATCGCGCGCGCTGG 352  
Qy 199 GCGCACCGCGCTCGCGCGCGGTCAATTTGCGCGTCTATTTCCGCGGAGCGACCGCG 258  
Db 353 GCGCACCGCGCTCGCGCGCGGTCAATTTGCGCGTCTATTTCCGCGGAGCGGCTGG 412  
Qy 259 CGGCGCTCTGCGCTCTCGCGCGCGGTCAATTTGCGCGTCTATTTCCGCGGAGCGACCGCG 318  
Db 413 CGTCTGAGCGCTCTGCTCTCGCGCGCGGTCAATTTGCGCGTCTATTTCCGCGGAGCGG 449  
Qy 319 GTTCATCAGCTTTGCGTGGCGCGCGCGCGCTTTTGGGCGCTGCAATTTAAGTTTGTGA 378  
Db 450 ----- 449  
Qy 379 CTGGGGCAAAATCTCTGAGAGTAGGCTGACCGAGAGAGGTTCCTCTGAGCCCTGATGAT 438  
Db 450 -----GGATAGGCTGACCGAGAGAGGTTCCTCTGAGCCCTGATGATGATGATGAT 492  
Qy 439 CGGACCGGGAAGCTGTGGCATGCTTCATCGAAGG---CGAGCTGCACAAATGCTTTAC 495  
Db 493 CGAAGCGGAAACGTGTGGCATGCTTCATCGAGGAGCGAGCTGCAGCGGATGCTCTGC 552  
Qy 496 GGGTACAGTTGCGACGCGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 555  
Db 553 GGATACAGTTGCGATGGCGTGTTCGCGCGCGGTGCTGAGCGCGGACAGTACTAGCTGTG 612  
Qy 556 GTCGTGGTGGATCTTATGCTAAGCGAGTATAGCGCGAGGAGTGGTGTTCAGCG 615  
Db 613 GTTGTGGTGGATCTTATGCTAAGCGAGTATAGCGCGAGGAGTGGTGTTCAGCG 672  
Qy 616 CGTGGTAAATGCTGGCTCAGATGGCTGGCATGATCCCTCTTCCATATAGCACGTTT 675  
Db 673 CCGTGGTGGTGGTGGTGGCTCAATGGCTGGTATGATCCCTCTTCCATATAGTAT 732  
Qy 676 GATTGGGAAGCGGACCT 735  
Db 733 GATTGGCAAGGTGACCTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 792  
Qy 736 CACTTGGTGGATTCAGCAAGCATGATTCAGCAATGTAGAACATCCCGGTACTTTTCT 795  
Db 793 CATTGGCTGGATTCAGCAAGCATGATTCAGCAATGTAGAACATCCCGGTACTTTTCT 852  
Qy 796 GGAGCTGTGCGAAGCTTGACTTATTTGAAGAGCTTGGAGTTAATTTGAATTAATG 855  
Db 853 GGTGCTGTGCAAGCTTGACTTATTTGAAGAGCTTGGAGTTAATTTGAATTAATG 912  
Qy 856 CCCTGCCATGAGTTCAAGCGGCTGAGTCAACCTCTTCTTCCCAAGATGAACTTTGG 915  
Db 913 CCCTGCCATGAGTTCAAGCGGCTGAGTCAACCTCTTCTTCCCAAGATGAACTTTGG 972  
Qy 916 GGATATTTCCCAATAAACTTTTTCACCAATGCAAGATACACATCAGCGGGGATAAAA 975  
Db 973 GGATATTTCCCAATAAACTTTTTCACCAATGCAAGATATTTCTTCAAGTGGCATAAGA 1032

QY	976	AAC	TGTTGGGCGGTGAATGCCATAAATGAGTTCAAAACCTTTTGTAAGAGAGGGCTCACAACCGG	1035
Db	1033	GAC	TCCTGATGTGCTGTGCATAAATGAAATTAAAGACTTTTGTTAAAGGAGAGGCCCAACAACGG	1092
QY	1036	GGA	ATTGAGGATGATCCCTGGATGTTTGCTTCAAACCATACAGCTGAGGGGTAAATGAGAATGGT	1095
Db	1093	GGA	ATTGAGGATGATCATGGATGTTTGCTTCAAATCATACAGCTGAGGTAAATGAGAAGGC	1152
QY	1096	CCA	ATATATATCAATTTAAAGGGGTCGATAATACTACATACATATATGCTTTGCAACCCAAAGGGA	1155
Db	1153	CCA	ATATATATCTTTTAGGGGATAGATAATAGTAGTACATACATGCTTTGCACCTTAAGGGA	1212
QY	1156	GAG	TTTTTATACATATCTGCTGTGGGAATACCTTCAACTGTAATCATCTGCTGGTTCGT	1215
Db	1213	GAG	TTTTTATATATATCTGCTTTGGGAAATACCTTCAATTGTAATCATCTGTAGTCCGT	1272
QY	1216	CAAT	TCATTTGATGTTTAAAGATCTGGGTGACCGAAATGCAATGTTGATGGTTTCGT	1275
Db	1273	CAAT	TTTATAGTGGATTCGTTGAGATACCTGGTAAACAGAAATGCATGTTGATGGTTTCGT	1332
QY	1276	TTT	GATCTCCATCATAANTGACAGAGGTTCCAGTCTGTGGGATCCAGTTTAAACGTGAT	1335
Db	1333	TTT	GACCTTGCATCTATAGTACAGAGGATGCACTTATGGGATCAGTTAATGTGTAT	1392
QY	1336	GGAG	CTCCAATPAGAAGTGATGATCACAAACAGGACACCTCTGTTACTCCACCACATT	1395
Db	1393	GGA	ATCCAATGGAAGTGATGATTACGACAGGGACACCTCTGTTGCCCCAACCACTT	1452
QY	1396	ATT	CACATGATCAGCAATGACCCNAATTTCTTGGAGGCTCAAGCTCATCTGCTGAAGCATGG	1455
Db	1453	ATT	GACATGATTAGCAATGACCCAAATTTCTTGGAAATGTCAGGCTCATGCTGAAGCATGG	1512
QY	1456	GAT	GACGAGGCGCTCTATCAAGTAGGTCAATTTCCCTCACCTGGAATGTTTGGTCTGAGTGG	1515
Db	1513	GAT	GACGAGGCTCTATCAAGAAGGTCAGTTTCTCTCACTGGAACGTTTGGTCAGAGTGG	1572
QY	1516	AAT	GGAAGTACCGGACATTTGCTGCTCAATTCATTAAGGCACTGATGAAATTTGCTGGT	1575
Db	1573	AAT	GGAAGTATCGCGATACCGTGCCTCAGTTTCATCAAGGCCACAGATGATTTGCTGGT	1632
QY	1576	GGT	TTTCCCAAGTCTTTGCTGGAAGTCCACACCTATACCAAGGTAACTTTGTGGCAATACT	1635
Db	1633	GC	TTTTGCTGAAATGCTATGGAAGTCCACAGTTATAC-----	1671
QY	1636	TG	TAAATGAGTTGAGTGAATGTCACTGGATTTTTTATATATATACCATGATGATACACA	1695
Db	1672	----	-----	1671
QY	1696	TCT	AAAAATATAACAATCATAGTATGTCATATGCAATTTGGCTTAAGAAGATTAGTGAT	1755
Db	1672	----	-----	1671
QY	1756	AC	ACTAGTGCTATATATAGGTTTTTAAACCCAACTTCCCAATGAAGAAATAGGCGCTTT	1815
Db	1672	----	-----	1671
QY	1816	CT	AGTTATCTATTATTTTGTCCGTGAATAATCCACTGAAAAATCCAGCCATGTCATT	1875
Db	1672	----	-----	1671
QY	1876	TTTT	PAGGGGGAGAGAAACTATTTGATTTGCCCCCCTTAAAGAAGCAATCTCAAAAT	1935
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QY	1936	TC	ATAGTAAAGTTGCTTTTCTGTAAAGAAAGGAAAAACGACTTCATATCTTCTATCGGTGC	1995
Db	1672	----	-----	1671
QY	1996	TAA	CTTAGCTCGATGATATATTTGATGAATGCAATGCCCCAAATTTAATTTGTCGGATAAATTG	2055
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QY	2056	ATCTGTTATTTCACAAATTTCTCTATTGGTTCTCTAGAAATCAAAACGATGAACCTTGTTATT	2111
Db	1672	-----	1671
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Db	1672	-----CAGGACGGGGGAGAGACCTTGGCACAGTATCG	1705
QY	2176	ACTTTGTATGTGCACATGATGGATTTACACTGGCTGATTTTGGTAAACATATAAGAAAGT	2235
Db	1706	GCITTTGTATGTGCACACAGATGGATTTACACTGGCTGATTTTGGTACATACAATAGCAAAGT	1765
QY	2236	ACAAATTTACAAATGGGGAGCAACACAGAGATCGAGAGAAATCAAACTCTTGTAGCTGGAATT	2295
Db	1766	ACAATCTGTCAAATGTGAGAGCTTCAGAGATGGGHAATAATATCTTGTAGCTGGAATT	1825
QY	2296	GTGGGAGGAGAGAAATTCGCAAGATTGTCTGTCAAAGATTGAGGAAGACGACATGC	2355
Db	1826	GTGGGAGGAGAGAAATTTGCAAGTCTGTGCACTCGAAGATTAAGAGGAGGCAAAATGC	1885
QY	2356	GCAATTTCTTTGTTGTCTCATGGTTTCTCAAGGAGTTTCCAAATGTTCTACATCGGTGATG	2415
Db	1886	GCAATTTCTTTGTTGTCTTATGGTTTCTCAGGAGTTTCCAATGTCTCATATGGGCGATG	1945
QY	2416	AAATATGCCACACAAAAGGGGGCAACAAACAATACATACTGCCATGATTTCTTATGTCAAAAT	2475
Db	1946	AAATATGCTCACAAAGGGAGGGAACAACAATACGTACTGCCATGACCATTATGTCAAAAT	2005
QY	2476	ATTTTCTCGTGGATATAA---AAGAACATACTCTGAGTTGTGACCCGATTTCTGCTGCCTCA	2532
Db	2006	ATTTCCCTTTGGGATAGAAGAGAGAAACAATCTCTGATTTGTACAGATTTCTGCCGCTCTCA	2065
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Db	2066	TGACCGAATTTCCGCAAGAATGTGAATCTCTTGGCCTTGAGGACTTCCCGACTTCAGAAC	2125
QY	2593	GGCTGACGTGECATGTCATCAGCCTGGGAAGCCTGATTTGCTGTGAAATAGCCGATTCG	2652
Db	2126	GGTTGAAATGGCACGGTTCATCAGCCCGGAAGCCTGACTGCTCAGAGGCAAGCCGATTCG	2185
QY	2653	TTGCGCTTTCCATGAAGAATGAAGACAGGGCAGATCTATGTGGCTTCAACACACAGCC	2712
Db	2186	TTGCGCTTCCATGAAGGAGAAACCAAGGCAGATCTACGTGGCTTCAACACACAGTC	2245
QY	2713	ACTTACCGGCCGTTGTTGAGCTCCACAGCGCCAGGGCGCCGGTGGGAACCGTGGTGG	2772
Db	2246	ACCTTCCGGTGGTTGTTGGCTTCCAGAGCGCTCTGGGTTCCGATGGAGCCGGTGGTGG	2305
QY	2773	ACACAGGCAAGCAGACACATAGACTTTCTCTACCCAGCAGCTTACTGTATCGGGCTCTCA	2832
Db	2306	ACACCGGCAAGGAGGCAACCATATGACTTCTCTACCGATGGCCGAGTCTGGTGTGTCA	2365
QY	2833	CCATACACCAAGTCTCGCATTTCTCTACTTCCAACTCTACCCCATGCTCAGCTACTCAT	2892
Db	2366	CCGCTTACCAAGTCTCTCATTTCTCTCAATCTCAATCTCTATCTCTATCTCTCAGCTACTCT	2425
QY	2893	CGGTCACTCTAGTATTTGGGCCCTTGATGTTTGAGAGACCAATATATA	2938
Db	2426	CCATCACTCTTGATTTGGCCCTTGATGCTCTGAAAGAGCAGATATACA	2471

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RESULT 3
US-09-463-238-2
; Sequence 2, Application US/09463238
; Patent No. 6469230
; GENERAL INFORMATION:
; APPLICANT: Edwards, Elizabeth A
; APPLICANT: Smith, Alison M
; APPLICANT: Bustos Guillen, Regla
; APPLICANT: Martin, Catherine R
; APPLICANT: Plant Bioscience Limited
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 97.118

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; CURRENT APPLICATION NUMBER: US/09/463,238  
; CURRENT FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/02280  
; PRIOR FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: GB 9716185.5  
; PRIOR FILING DATE: 1997-07-31  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2706  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2641)  
; OTHER INFORMATION: n = a or g or c or t  
US-09-463-238-2

Query Match 22.5%; Score 673.2; DB 4; Length 2706;  
Best Local Similarity 69.4%; Pred. No. 3.3e-149;  
Matches 937; Conservative 0; Mismatches 398; Indels 15; Gaps 1;  
QY 395 AGGATAGGTGACCGAGGAGTCCCTTGACCCCTGATCAATCGACCGGAGACGTGT 454  
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QY 455 GCGATGCTTCATCAAGGCGAGCTGCACACATCTTTACGGGTACAGGTTGACGGCA 514  
DB 485 GCGATGCTTCCTTAAGGAGATTTGAGAATATGCTATATGCTACAAATTTGATGGA 544  
QY 515 CTTTGTCTCTCACTGCGGGACACTACCTTGATGTTTCCATGTTCCATGTCGTGGATCCTTATG 574  
DB 545 AATTCTGTCTCTCAAGAGGACACTACTTGTGACTCTTCGCGAGATAGTGTGGATCCTTATG 604  
QY 575 CTAAGGCGAGTGATAAGCGGAGGAGTATGGTGTTCAGGCGGTGGTAAACAATTGCTGGC 634  
DB 605 CCAAGGCTATAGTAAGCAGAGGAGATATGGTGTATTAGGCGCAGAGTATGTTGGC 664  
QY 635 CTCAGATGCGTGGCATGATCCCTCTTCCATATAGCAGCTTTGATTTGGAAAGGCGACCTAC 694  
DB 665 CCCCAATGGCTGGCATGGTACCTTCTGCTTCTGATCAGTTTGAATTGGAAGAGATCTAC 724  
QY 695 CTCATAGATATCTCAAGAGACCTGGTATATATAGATGCACTTGCCTGGATTCACGA 754  
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QY 755 AGCATGATTCAAGCAATGTAGAACATCCGGTACTTTTCATTTGAGCTGTGTGCAAGCTTG 814  
DB 785 ATCATGAGTCGAGTGAACAAATATCTCTGTACTTACCTTGGTGTGTGGAGAACTTG 844  
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QY 920 ATTTACCATAACTCTTTTTCACATGACAGATACATCATCAGGCGGATATAAAACT 979  
DB 965 ATTTACTGTCAATTTCTTCTCCAATGGGAAGATACATCTCTGCTGTCTAAGTAAT 1024  
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DB 1085 TCGAGGTATCATGGATGTTGTTTCACTACACTGTGTAAGGAAATGAAATGTTCCCA 1144  
QY 1100 TATTATCAATTTAAGGGGTGATTAATCTATACATCTATGCTTGCACCCCAAGGAGAT 1159  
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QY 1160 TTTATAACTATTCTGGCTGGGATACCTTCAACTGTAATCATCTCTGTGGTTCGTCAAT 1219  
DB 1205 TTTACAACTACTCAGGATGGGAAATACCTTCACTGTAATTAATCCCATTTGACGTCAAT 1264  
QY 1220 TCATTGTAGATTGTTTAAAGATACTGGGTGACGGAATCATGTTGATGTTTTCGTTTG 1279  
DB 1265 TTTATAGTGATTGCTTGAGATATTGGGTTTACCGAAATGACGTAGATGGCTCCGCTTTG 1324  
QY 1280 ATCTTGCATCCATTAATGACCAAGAGGTTCCAGTCTCTGGGATCCAGTTAACTGATGGAG 1339  
DB 1325 ATCTTGTCTTCTATCTTACAAGAGTAGCAGCTCTGTGAATGCTGTAATGCTATGGAA 1384  
QY 1340 CTCCAATAGAGGTTGACATGATCAACAGGAGGACACCTCTCTTACTCCACCACCTTATTG 1399  
DB 1385 ATTCAATTGACGTTGACGTGATCACCACAGGCACCTCTCTCACAAGCCCAACCATTTG 1444  
QY 1400 ACATGATCAGCAATACCCCAATCTTTGGAGGGCGTCAAGCTCATTTCTCTGAAGCATGGATG 1459  
DB 1445 ATATGATTAGCAATGATCCAATACTTCTGGGAGTAAGCTTATAGCTGAAGCATGGGAT 1504  
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QY 1520 GGAAGTACCGGACATTTGCGTCAATTCATTTAAAGGCACTGATGGATTTGCTGGTGT 1579  
DB 1565 GAAAGTACCGTACATGTTGACGCGAGTTTCAATCAAGGCACTGATGGGTTTCTGGGGCTT 1624  
QY 1580 TTGCGCAATGCTTTTGGAGTCCACACCTATACAGGTAAGTTGTGCAATCTTCTGA 1639  
DB 1625 TTGTCGAATGCCCTTTGGAGGCCCAATCTATATACAGAAAGGAGGAGAAACCATGGA 1684  
QY 1640 AATGAGTTGAGTGAATGTCACCTGGATTTTATATATATACCAATGATGATACATCTA 1699  
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DB 1745 ACAATAAACACAAATTTGGCAATGGAGAGG 1774

RESULT 4  
US-09-463-238-11  
; Sequence 11, Application US/09463238  
; Patent No. 6469230  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Elizabeth A  
; APPLICANT: Smith, Alison M  
; APPLICANT: Bustos Guillen, Regla  
; APPLICANT: Martin, Catherine R  
; APPLICANT: Plant Bioscience Limited  
; TITLE OF INVENTION: Starch Debranching Enzymes  
; FILE REFERENCE: 97.118  
; CURRENT APPLICATION NUMBER: US/09/463,238  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/02280  
; PRIOR FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: GB 9716185.5  
; PRIOR FILING DATE: 1997-07-31  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 2806  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (822, 826, 2707 and 2797)  
; OTHER INFORMATION: n = a or g or c or t  
US-09-463-238-11

Query Match 20.5%; Score 613.2; DB 4; Length 2806;

Best Local Similarity 68.0%; Pred. No. 4.9e-135; Matches 922; Conservative 0; Mismatches 410; Indels 24; Gaps 4;

QY 395 AGGATAGGGTACCGAGGAGGTTCCCTTTCACCCCTGATGAATCGGACCGGGAACGTGT 454  
Db 488 AGAAGAGAGTACCGAGCAAAATTTCTCTGGATCCTCTAGCTAATAAACTGGAGATGTAT 547  
QY 455 GGCATGCTTTCATCGAAGGCGAGCTGCACAACATGCTTTACGGGTACAGGTTTCGACGGCA 514  
Db 548 GGCATGCTTTCATCGAAGGCGAGATTTGAGAAATATGCTATATGCTACAAAATTTGATGGGA 607  
QY 515 CTTTGTCTTCCTCACTGCGGGCAGCTACCTTGTATGTTTCCAAATGCTGCTGGTGGATCCTTATG 574  
Db 608 AATTCTGCTCTGAAGAAGGACACTACTTTGACTCTTCGCAGATAGTGTGGATCCCTTATG 667  
QY 575 CTAAGGCGATGATAAGCGGAGGAGTATGCTGTTCCAGCGCGTGGTAACTTGTCTGGC 634  
Db 668 CCAAGGCTTATAGTAAGCAGAGAGATATGCTGTATTAGGGCCAGAGGATGATTTGTGGC 727  
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QY 749 TCAGGAGCATGATTCAGCAATGTAGAACATCGGCTACTTTCATTTGAGGCTGTGCGA 808  
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QY 809 AGCTTGTACTTTTGAAGGAGCTTGGAGTAAATTTGATTTGAATTAATGCCCTGGCATGAGT 868  
Db 908 AACTTGTATCACTTGAAGGAACCTTGGTGTCAACTGTATAGAGTAATGCTCCCTGTACGAGT 967  
QY 869 TCAAGGAGCTGGAGTACTCAACCTTCTCTC-----CAAGATGAATTTT 913  
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QY 914 GGGATATTTACCAATAAATCTTTTCCAAATGACAAGATACACATCAGGCGGGATAA 973  
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QY 974 AAAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGAAGAGGCTTCAAAAC 1033  
Db 1088 GTAATTCGGGCTCGGTGCAATAAACAATTTAAGTATCTTGTCAAGGAAGCACATAAAC 1147  
QY 1034 GGGGAATTTAGGTCATCTGATGCTCTTCAACCATACAGCTGAGGGTAATGAGAATG 1093  
Db 1148 GTGAATTCGAGGTTATCATGATGCTGTTTTCATCATCATCTGCTGAAGGAATGAATG 1207  
QY 1094 GTCCAAATATATATTTAAGGGGTGCGAATAATACATACATACTATATCTTTGCCACCAAGG 1153  
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QY 1154 GAGAGTTTATTAATCTTCTGGCTGGGAATACCTTCACTGTATCATCTCTGCTGTTTC 1213  
Db 1268 GTGAATTTTCAACTACTCAGGATGTGGAAATACCTTCACTGTATTAATTTCCCATTTGTAC 1327  
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Db 1445 ATGGAATTCATTTGAACGCTGACGTGATCAACAGGCACTCTCTCTCAAGGCCACCAT 1504  
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Db 1565 GGGATTTGGAGGCTTTTACCAAGTTGGCATGTTTCCGCACCTGGGTATCTGGTGGAGT 1624  
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QY 1574 STGGTTTTGCCAATGCTTTTGTGGAAGTCCACACCTATACCAAGTAAGTTGTGGCAATA 1633  
Db 1685 GGGCTTTTGTCTGAATGCTTTTGTGGAAGCCCAATCTATACCAAGAGGAGGAGAAAC 1744  
QY 1634 CTTGTAATGAGTTGAGTGAATGTCACCTGGATTTTATATATATACCACTGATGATACA 1693  
Db 1745 CATGGAACAGTATAAATTTCTGTTGTCGCCAGATGGTTTACTTTGGCTGATTTAGTGA 1804  
QY 1694 CATCTAAATATATAACAATCATAGTGTATGCAATG 1729  
Db 1805 CATACAACAATAAACACAAATTTGGCAATGGAGAGG 1840

RESULT 5  
US-09-187-124-1  
; Sequence 1, Application US/09187124A  
; Patent No. 6255563  
; GENERAL INFORMATION:  
; APPLICANT: Emmermann, Michael  
; APPLICANT: Kossman, Jens  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES  
; TITLE OF INVENTION: FROM POTATO  
; FILE REFERENCE: GFB8  
; CURRENT APPLICATION NUMBER: US/09/187,124A  
; CURRENT FILING DATE: 1998-11-05  
; EARLIER APPLICATION NUMBER: PCT/EP97/02292  
; EARLIER FILING DATE: 1997-05-06  
; EARLIER APPLICATION NUMBER: DE 196 18 125.9  
; EARLIER FILING DATE: 1996-05-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2133  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(1819)  
; OTHER INFORMATION: Clone: Isos5  
US-09-187-124-1

Query Match 19.2%; Score 575.4; DB 3; Length 2133;  
Best Local Similarity 69.8%; Pred. No. 3.6e-126;  
Matches 799; Conservative 0; Mismatches 331; Indels 15; Gaps 1;

QY 600 GTATGCTTTCAGCGGCTGGTAACTTGTGCGCTCAGATGCTGGCATGATCCCTCT 659  
Db 1 GAATTCGGCAAGGCGGCGAGGATGATTTGGCCCCCAATGGCGCATGGTACCTTC 60  
QY 660 TCCATATAGCAGCTTTGATTTGGGAAGGCGACCTACCTCTTAAGATATCCTCAAAAGGACCT 719  
Db 61 TCGTTCTCATCAGTTTGTATTGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGATCT 120  
QY 720 GGTATATATGAGATGCACTTGGTGGATTCCAGAGCATGATTTCAAGCATGTAGACA 779  
Db 121 TGTAACTATGAATGCAATGCTTGGGATTTTCAAAATCATGAGTCGAGTGAACAAATA 180  
QY 780 TCCGGGTACTTTCAATTGGAGCTGTCTCGAAGCTTGACTATTTGAAGGAGCTTTGAGGTTAA 839  
Db 181 TCCTGTTACTTACCTTGGTGTGTGGAGAACTTGATCACTTTGAAGGAACCTTGGTGTCAA 240  
QY 840 TTGTTATTGAATTAATGCTCCCATGAGTTTCAAGAGCTGGAGTACTCAACCTCTTCTTC 899



Db 721 TAGCAGCTCGTGGAAATGCTGTAATGTCTATGGAAATTCAAATTGACGGTGACATGATCAC 780  
QY 1365 AACAGGGACACCTCTTGTACTCCACCACTTATTGACATGATCAGCAATGACCAATTCCT 1424  
Db 781 CACAGGCACTCTCTCACAGCCACCACTGATTGATATGATTAGCAATGATCCATACT 840  
QY 1425 TGGAGGCGTCAAGCTCATGCTGAAGCATGGATGCGAGGCGCTCTATCAAGTAGGTCA 1484  
Db 841 TAGTGGAGTAAGCTTATAGCTGAAGCATGGATGCTGGAGCGCTTTTACCAAGTTGGCAT 900  
QY 1485 ATTCCCTCACATGGAATGTTGGTCTGAGTGAATGGAAGTACCGGACACATTTGGGTCA 1544  
Db 901 GTTTCGGCACTGGGGTATCTGGTCGGAGTGAACCGGAAGTACCGTGACATGGTAGGTCA 960  
QY 1545 ATTCAATAAGGCACTGATGATTTGCTGGTGGTGTTCGCGAATGCTTTTGTGGAAGTCC 1604  
Db 961 GTTCATCAAGGCACTGATGGTCTTCTGGGCTTTTGTGCTGAATGCCCTTTGTGGAAGCCC 1020  
QY 1605 ACACCTATACAGTAAGTTGTGCAATACCTTGTAAATGAGTTGAGTGAATGTCACCTGG 1664  
Db 1021 AAATCTATACAGAAAGGAGGAAGAAACCATGGAAACAGTATAAAATTCGTGTGCCCCA 1080  
QY 1665 ATTTTATATATACCATGATGATACATCTAAATATATATACCAATCATAGTGTATGC 1724  
Db 1081 CGATGGTTTACTTGGCTGATTTAGTGACATACACAAATTTGCAAAATGG 1140  
QY 1725 ATATG 1729  
Db 1141 AGAGG 1145

## RESULT 7

US-09-463-238-3

; Sequence 3, Application US/09463238

; Patent No. 6469230

; GENERAL INFORMATION:

; APPLICANT: Edwards, Elizabeth A

; APPLICANT: Smith, Alison M

; APPLICANT: Bustos Guillen, Regla

; APPLICANT: Martin, Catherine R

; APPLICANT: Plant Bioscience Limited

; TITLE OF INVENTION: Starch Debranching Enzymes

; FILE REFERENCE: 97.118

; CURRENT APPLICATION NUMBER: US/09/463,238

; CURRENT FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: PCT/GB98/02280

; PRIOR FILING DATE: 1998-07-30

; PRIOR FILING DATE: 1997-07-31

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 2634

; TYPE: DNA

; ORGANISM: Solanum tuberosum

US-09-463-238-3

Query Match 5.0%; Score 149.2; DB 4; Length 2634;

Best Local Similarity 51.0%; Pred. No. 1.6e-25;

Matches 633; Conservative 0; Mismatches 508; Indels 99; Gaps 8;

QY 412 GAGGTCCCTTGACCCCTGATGAATCGACCGGGAACGTGGCAATGCTTCATCGAA 471  
Db 434 GAATTAGCATTTGGATCCACAGAAAGAACCCACAGGACATATGGCACATATGCAATAG 493  
QY 472 GGCAGCTGCA--CAACATGCTTTACGGGTACAGGTTCCACGCGACCTTTGCTCCTAC 528  
Db 494 GAGTTGCCCAAGGTGTGCTTTATGGTTATCGCAATTGATGCACTCGAAATGGCAT 553  
QY 529 TGCAGGCACTACCTTGATGTTTCCAAATGCTGCTGGTGCATCCTTATGCTAAGGCAGTGATA 588  
Db 554 GAAGGGCATCGATTTGATGATAGCATTAATTTGGTTGATCCTTACGAAAACTAATTGAA 613

RESULT 8  
US-09-198-452A-1  
Sequence 1, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Griffiths, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
TITLE OF INVENTION: and treatment of infection  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1  
LENGTH: 1230025  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(15000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (15001)..(30000)  
OTHER INFORMATION: n=a or c or g or t  
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OTHER INFORMATION: n=a or c or g or t  
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OTHER INFORMATION: n=a or c or g or t  
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NAME/KEY: misc feature  
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OTHER INFORMATION: n=a or c or g or t  
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OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature  
LOCATION: (615001)..(630000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature



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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

Query Match 4.8%; Score 143; DB 4; Length 1230025;
Best Local Similarity 55.3%; Pred. No. 7.5e-23;
Matches 359; Conservative 0; Mismatches 260; Indels 30; Gaps 3;

QY 671 CGTTTGGAGGCGACCTACCTCTAAGATATCTCAAGAGGACCTGGTAATATATG 730
DB 446195 CATTTCTTGGATGGATCAGCCCTGCTATTCGCGAAGAGAGATCATCTATG 446254
QY 731 AGATGCACTTGGTGGATTCAGAGCATGATTCAGAGCATGTAGAACATCCGGTACTT 790
DB 446255 AGATGCACTGACGTTCCTTCACGCAATCTTCTCATCTAGGGTTCATGTCCGGGAACCT 446314
QY 791 TCATTGGAGCTGTCTCAAGCTTGACTATTGAAGGAGCTTGAGATTAAATTGATTGAAT 850
DB 446315 TCCTAGGATCATTGAAAGATCGACCATCTGCTAAGCTGGGAATCAACGCTGTGAC 446374
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QY 851 TAATGCCCTGCCATGAGTTCAACGAGCTGGAG-----TACTCAACCTCTCTTT 898
DB 446375 TCTTACCTATCTTTGAGTTCCATGAGACTGGCATCTCTTTTAGAAATTCGAATTCCTT 446434
QY 899 CCAAGATGAACCTTTTGGGATATTCTACCAATAAACTCTTTTCCAAATGACAATACA 958
DB 446435 ATCTGTGCAATATTGGGGTTATGCTCCCTAAATTTCTTTTCTCTTGGCGAGCTTATG 446494
QY 959 CATCAGGGGGGATAAAAAATCTGTGGCGCTGATGCCATAAATGAGTTCAAACTTTTGTAA 1018
DB 446495 CTTATGCC-----TCTGATCCTTGGCTCCCAAGTAGAGAGTTTAAAACTTTAGTAA 446545
QY 1019 GAGAGGCTCAAAACGGGGAATTTGAGGTGATCCTGGATGTTGTCTTCAACCATACAGCTG 1078
DB 446546 AGACCTTGCATCAAGAAGTATTGAGGTCAATCTTTGATGTTGTTTAAATCATACGGCT 446605
QY 1079 AGGTAATGAGATGGTCCAAATATTATCATTTAAGGGGGTGCATAATACATACATACTATA 1138
DB 446606 TGC-----AAGGGACGACCTGCTCTTTGCTTGGATAGACACTCCGAGCTATTATA 446656
QY 1139 TGCCTGCACCAAGGAGAGTTTATTAATACTATTCTGGCTGTGGGAATACCTTCAACTGTA 1198
DB 446657 TTTTAGATGCACAGGTGCATTTACAATTAATTCAGGCTGTGGAAACACTCTCAATACAA 446716
QY 1199 ATCATCTCTGGTTCGTCATTAATTCATTTAGATGTTTAAAGATACCTGGGTGACGGAATGC 1258
DB 446717 ACCCGCCCCCAGCAACCAATGATTTCTCGACATCTTACGTTATTGGGTAGAGAAATGC 446776
QY 1259 ATGTTGATGTTTCTGTTTTCATCTTGCATCCATAATGACCAGAGGTTTC 1307
DB 446777 ATGTCGATGGGTTCGATTTGATCTTCTGCTTTCTTCTGCTGCTGCTC 446825
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## RESULT 9

```
US-09-463-238-12
; Sequence 12, Application US/09463238
; Patent No. 6469230
; GENERAL INFORMATION:
; APPLICANT: Edwards, Elizabeth A
; APPLICANT: Smith, Allison M
; APPLICANT: Bustos Guillen, Regla
; APPLICANT: Martin, Catherine R
; APPLICANT: Plant Bioscience Limited
; TITLE OF INVENTION: Search Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463.238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-09-463-238-12
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Query Match 4.3%; Score 129.6; DB 4; Length 1389;
Best Local Similarity 53.0%; Pred. No. 5.2e-21;
Matches 357; Conservative 0; Mismatches 299; Indels 18; Gaps 3;

QY 2155 GGAACCTTGGCAGCATGATCAACTTTGATGTCACATGATGGATTTTACACTGGCTGATT 2214
DB 474 GAAAGCCGTACCAAGTGTCAACTTCGTGATTCGCCCATGATGGCTTTTACCTTTGATGACC 533
QY 2215 TGGTAACATATAATAAGAAGTACAAATTTACCAATGGGGAGAACACACAGAGATGGAGAAA 2274
DB 534 TTGTTTATCATCAATAATAAAGCACAATGATCGAACCGTGAAGGTGGCAATGATGATGCA 593
QY 2275 ATCAATCTTAGCTGGAATTTGGGGAGGAGAGATTCGCAAGATTTCTCTGTCAAAA 2334
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QY 2263 GAGATGGAGAAATCAAACTTCTAGCTGGAATTTGGGAGGAGGAGAAATTCGCAAGAT 2322  
DB 1770248 CGCAGCGGGAAGCTACACCGATCTGTGGAACTCGGTGTGCGAGGGCCCAACGATGACC 1770189  
QY 2323 TGTCTGTCAAAAGATTTAGAGAGGAGGAGATGCGCAATTTCTTTTGTCTCATGGTTT 2382  
DB 1770188 CCGACATCTTGGCGCTGCTGCCCGCCAGATGCGCAACATGTGGGCCACGCTTATGGTCA 1770129  
QY 2383 CTCAGGAGTTCCAAATGTTCTACATGGTGTATGAATATGCCACACAAAGGGGCAACA 2442  
DB 1770128 GCCAGGGCACCCGATGATGCCACCGGAGAGATTTGGCGCACCAATACGGCAACA 1770069  
QY 2443 ACAATACATAGTCCATGATTTCTTATGTCAATTTTTCGCTGGGATFAAAAAAGACAAT 2502  
DB 1770068 ACAACGTCTAGTCCAGGACTCCGAATTTCTTGGATGGATTTGTCATTTGGTGCAAGA 1770009  
QY 2503 ACTCTGAGTTGCCAGGATTTCTGCTCATGACCAAAATTCGCAAGGAGTGGAGGGTC 2562  
DB 1770008 ATGCCGATCTGCTAGCTTTGCGACGAAGGCGAGCTTTGGCGAAGAACCAAGGTGT 1769949  
QY 2563 TTGGCC 2568  
DB 1769948 TTGGCC 1769943

RESULT 12  
US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: TUBERCULOSIS  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 3.4%; Score 102.8; DB 3; Length 4411529;  
Best Local Similarity 52.6%; Pred. No. 4.1e-13;  
Matches 224; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 2143 AGGAGGAGGAGAAACCTTTGGCACAGTATCACTTTGTATGTGCAATGATGATTTA 2202  
DB 1770242 AAGCAACCGCGCGCGCCAGTCCAGTATCAATTTCTGTCACCGCCACGAGGGTTCA 1770183  
QY 2203 CACTGGCTGATTTTGTAACTATTAATAGAGTACATTTTACCAATGGGAGCAACA 2262  
DB 1770182 CACTCAAGCCTGTTCTGTACACGACAGCAACAGAGGCAATGGCGAGAACACC 1770123  
QY 2263 GAGATGGAGAAATCACAATCTTAGCTGGAATTTGTGGGAGGAGGAGAAATTCGCAAGAT 2322  
DB 1770122 GCGACGGGGAAGCTACACCGATCGTGGAACTCGGTGTGCGAGGGCCCAACCGATGACC 1770063  
QY 2323 TGTCTGTCAAAGATTTGAGNAGAGGAGATGCGCAATTTTGTGTTCTCATGTTT 2382  
DB 1770062 CCGACATCTTGGCGCTGCGTCCCGCCAGATGCGCAACATGTGGGCCACGCTTATGGTCA 1770003  
QY 2383 CTCAGGAGTTTCCAAATGTTTCTACATGGGTGATGAATATGGCCACACAAAAGGGGGCAACA 2442  
DB 1770002 GCCAGGCGACCGCATGATCGCCACGCGACGAGATTTGGCGCACCCATACGCAACA 1769943  
QY 2443 ACAATACATAGTCCATGATTTCTTATGTCAATTTATTTCTGCTGGGATAAAAAGACAAT 2502

DB 1769942 ACAACGTCTACTGCGCAGGACTCCGAATTTATCTTGGATGGATTCATTTGGTGCAACA 1769883  
QY 2503 ACTCTGAGTTGACCGATTTCTGCTCATGACCAATTTCCGCAAGGAGTGGCGAGGTC 2562  
DB 1769882 ATGCCGATCTGCTAGCTTTGCGACGCAAGGCGAGACCTTGGCAAGAACCAAGGTGT 1769823  
QY 2563 TTGGCC 2568  
DB 1769822 TTGGCC 1769817

RESULT 13  
US-09-557-884-1  
; Sequence 1, Application US/09557884  
; Patent No. 6506581  
; GENERAL INFORMATION:  
; APPLICANT: Fleischmann et al.  
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3 1/2 inch diskette  
; COMPUTER: Dell Pentium  
; OPERATING SYSTEM: MS DOS v6.22  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/557,884  
; FILING DATE: 25-Apr-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/476,102  
; FILING DATE: JUN-5-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michelle S. Marks  
; REGISTRATION NUMBER: 41,971  
; REFERENCE/DOCKET NUMBER: PBI86P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1830121 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1

Query Match 3.0%; Score 88.8; DB 4; Length 1830121;  
Best Local Similarity 56.0%; Pred. No. 5.6e-10;  
Matches 168; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 987 TGATGCCATAATGAGTTCAAACTTTTGAAGAGGCTCACAAACGGGAATTTAGGT 1046  
DB 1439162 TAATCCATTTGGCTGAATTTAAACGATGTTAAAGCATTTTCAAAAGCAGGTCATTGAAT 1439221  
QY 1047 GATCCTGATGTTCTTCAACCATACAGCTGAGGTAATGAGATGGTCCAATATTATC 1106  
DB 1439222 TATTTAGACGTGGTATTAAACCATTCGCGAATCGAGCAAACTTACCCACATTCAG 1439281  
QY 1107 ATTTAAGGGGTCGATATACATACATCTATCTATCTTTCACCCAGGAGGATTTTATA 1166  
DB 1439282 CCAGGTGTATTTGATGATCAAACTTACTATTGGCGCAACGATCAAGGCGCTTATATCAA 1439341

QY 1167 CTATTCGGCTGGGAATACCTCAACTGTAATCATCTCTGGTTCGTCAATTCATTGT 1226  
Db 1439342 TTGACAGGCTGGCGCAATATGCTCAATTTATCTCTGATAGGGCGAAATGGGTGGT 1439401  
QY 1227 AGATTGTTTAAAGATACTGGGTGACGAAATGCCATGTTGATGGTTCGTTTTCATCTTGC 1286  
Db 1439402 GGAATGCTGGTTATTGGGTGGAGCAATGCCATATTGATGGATTCCGTTTTCATTAGC 1439461

## RESULT 14

US-09-643-990A-1

; Sequence 1, Application US/09643990A

; Patent No. 6528289

; GENERAL INFORMATION:

; APPLICANT: Robert D. Fleischmann

; Mark D. Adams

; Owen White

; Hamilton O. Smith

; J. Craig Venter

; TITLE OF INVENTION: The Nucleotide sequence of

; the Haemophilus influenzae Rd Genome, Fragments

; Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville,

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/643,990A

; FILING DATE: 23-Aug-2000

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/487,429

; FILING DATE: 1995-06-07

; APPLICATION NUMBER: 08/426,787

; FILING DATE: 1995-04-21

; ATTORNEY/AGENT INFORMATION:

; NAME: Kenley K. Hoover

; REGISTRATION NUMBER: 40,302

; REFERENCE/DOCKET NUMBER: PBI86P1C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-610-5790

; TELEFAX: 310-309-8439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1830121 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match 3.0%; Score 88.8; DB 4; Length 1830121;  
Best Local Similarity 56.0%; Pred. No. 5.6e-10;  
Matches 168; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 987 TGATGCCATAATGAGTTCAAACCTTTTGTAAAGAGAGGCTCACAAACGGGGAATTGAGGT 1046  
Db 1439162 TAATCCATTGGCTGAATTTAAACGATGGTAAAGGCTTTTCAAAAGCAGGCAATTGAAGT 1439221

QY 1047 GATCTGATGTTGTCCTTCAACCATACAGCTGAGGGTAATGAGATGGTCCATATTATC 1106

Db 1439222 TATTTAGCTGGTATTAAACCAATTCGCGAATCAGAGCAAACTTACCCACATTCAG 1439281

QY 1107 ATTTAAGGGGTCGATATACTACATACTATATGCTTGCACCAAGGAGAGTTTATAA 1166

Db 1439282 CCAGCGTGTATTGATGATCAAACTTACTATTGGCGCAACGATCAAGGCGTTATATCA 1439341  
QY 1167 CTAATTCCTGCTGGGAATACCTTCAACTGTAATCATCTCTGGTTCGTCAATTCATTGT 1226  
Db 1439342 TTGACAGGCTGGCGCAATATGCTCAATTTATCTCTGATAGGGCGAAATGGGTGGT 1439401  
QY 1227 AGATTGTTTAAAGATACTGGGTGACGAAATGCCATGTTGATGGTTCGTTTTCATCTTGC 1286  
Db 1439402 GGAATGCTGGTTATTGGGTGGAGCAATGCCATATTGATGGATTCCGTTTTCATTAGC 1439461

## RESULT 15

US-09-129-075-3

; Sequence 3, Application US/09129075

; Patent No. 6087149

; GENERAL INFORMATION:

; APPLICANT: Tsutsumi, No. 6087149iko

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Svendsen, Allan

; TITLE OF INVENTION: Starch Conversion Process

; FILE REFERENCE: 5262.204-US

; CURRENT APPLICATION NUMBER: US/09/129,075

; CURRENT FILING DATE: 1998-08-04

; EARLIER APPLICATION NUMBER: 0787/97

; EARLIER FILING DATE: 1997-07-02

; EARLIER APPLICATION NUMBER: 60/055,867

; EARLIER FILING DATE: 1997-08-13

; EARLIER APPLICATION NUMBER: PCT/DK98/00304

; EARLIER FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2181

; TYPE: DNA

; ORGANISM: Rhodothermus marinus

US-09-129-075-3

Query Match 2.7%; Score 80.6; DB 3; Length 2181;  
Best Local Similarity 49.6%; Pred. No. 2.3e-09;  
Matches 206; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 2172 ATCACTTTGTATGTGCACATGATGGATTACCTGGCTGATTTGGTAACATATAAAG 2231  
Db 1378 ATCAACTTCCTCACGGCGCACACGGCTTCACGCTGGAAGACCTGGTCAGCTACACGAAA 1437

QY 2232 AAGTACAATTTACCAATGGGAGAAACACAGAGATGGAGAAATCACAATCTTAGCTGG 2291

Db 1438 AAGCACACGACGAGATCTGGAAGCAACCGGACGCGATGACGAAACTACGACG 1497

QY 2292 AATTGTGGGAGGAGGAAATTCGCAAGATTGTCTGTCAAAGATTGAGGAAGGCGAG 2351

Db 1498 AACTGCGGGTGGAGGGACCCACGAGGATCCGCTCCGCTGGCCCTCGCGGAAGCGCTC 1557

QY 2352 ATGCGCAATTTCTTTTGTCTCATGTTTCTCAAGGAGTTTCCAAATGTTCTACATGGGT 2411

Db 1558 AAGCGCAGCTGATCAGCAGCTCTTTCTCTCGAGGGGCTGCCCATGCTGCTGGCGCGC 1617

QY 2412 GATGATATATGGCCACACAAAAGGGGCAACAAATACATACATGCTCCATGATTTATGTC 2471

Db 1618 GACGAGCTGCGCGACGCGACGACGCGCAACAAACGCGCTATTGCGAGGCAACAGAGATC 1677

QY 2472 AATTATTTTCGCTGGGATATAAAGAAACAAATACTGTGATTCACCGATTTCTGCTGCCTC 2531

Db 1678 AGCTGTACAACTGGCGAGCTCCACACGCGCAAGACGAGCTTTCTGGAGTTCGTGGCGCAG 1737

QY 2532 ATGACCAAAATTCGGAAGGAGTTCGAGGGTCTTGGCCCTTGAGGACTTTTCCAAACGG 2586

Db 1738 ACGATCTGGTTTCGACAGCAGATCGAGCTTCGCGGCGCGCAATTTCTGACCG 1792

Search completed: August 9, 2004, 22:08:05

Job time : 237 secs





; LOCATION: (2145)...(2960)									
; OTHER INFORMATION:									
US-10-238-091-1									
Query Match 100.0%; Score 2997; DB 15; Length 2997;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2997; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	G	G	T	C	G	G	G	G
DB	1	G	G	T	C	G	G	G	G
QY	61	T	C	G	G	G	G	G	G
DB	61	T	C	G	G	G	G	G	G
QY	121	A	G	A	C	G	A	G	A
DB	121	A	G	A	C	G	A	G	A
QY	181	G	A	A	T	C	G	G	G
DB	181	G	A	A	T	C	G	G	G
QY	241	C	G	G	G	G	G	G	G
DB	241	C	G	G	G	G	G	G	G
QY	301	G	G	T	C	G	G	G	G
DB	301	G	G	T	C	G	G	G	G
QY	361	T	G	C	A	A	T	T	G
DB	361	T	G	C	A	A	T	T	G
QY	421	C	T	T	G	A	C	G	G
DB	421	C	T	T	G	A	C	G	G
QY	481	C	A	A	C	A	T	G	A
DB	481	C	A	A	C	A	T	G	A
QY	541	C	T	T	G	A	C	G	G
DB	541	C	T	T	G	A	C	G	G
QY	601	T	A	T	C	G	G	G	G
DB	601	T	A	T	C	G	G	G	G
QY	661	C	A	T	A	G	A	C	A
DB	661	C	A	T	A	G	A	C	A
QY	721	G	T	A	T	A	G	A	C
DB	721	G	T	A	T	A	G	A	C
QY	781	C	G	G	G	G	G	G	G
DB	781	C	G	G	G	G	G	G	G
QY	841	T	G	T	A	T	A	G	A
DB	841	T	G	T	A	T	A	G	A
QY	901	A	A	G	A	T	A	G	A
DB	901	A	A	G	A	T	A	G	A
QY	961	T	C	A	G	G	G	G	A
DB	961	T	C	A	G	G	G	G	A





Db 721 GTAATATATGAGATGCACTTGGTGGATTACGAGCATGATTCAGCAATGTAGAACAT 780  
Qy 781 CCGGTACTCTTCATTGGAGCTGTGCGAAGCTTGACATATTTGAAGGAGCTTGGAGTTAAT 840  
Db 781 CCGGTACTCTTCATTGGAGCTGTGCGAAGCTTGACATATTTGAAGGAGCTTGGAGTTAAT 840  
Qy 841 TGTATTGAATTAATGCCCTGCCATGAGTTCAACGAGCTGAGTACTCAACCTCTTCTCC 900  
Db 841 TGTATTGAATTAATGCCCTGCCATGAGTTCAACGAGCTGAGTACTCAACCTCTTCTCC 900  
Qy 901 AAGATGAACCTTTGGGATATCTTACCAATAAATCTCTTTTCAACCAATGACAAGATACACA 960  
Db 901 AAGATGAACCTTTGGGATATCTTACCAATAAATCTCTTTTCAACCAATGACAAGATACACA 960  
Qy 961 TCAGCGGGATATAAAAACTGTGGCGGTGATGCCAATAAATGAGTTCAAACTTTTGTAA 1020  
Db 961 TCAGCGGGATATAAAAACTGTGGCGGTGATGCCAATAAATGAGTTCAAACTTTTGTAA 1020  
Qy 1021 GAGGCTCACAAACCGGGAATGAGGTGATCCTGATGTTCTTCAACCAATACAGCTGAG 1080  
Db 1021 GAGGCTCACAAACCGGGAATGAGGTGATCCTGATGTTCTTCAACCAATACAGCTGAG 1080  
Qy 1081 GGTAATGAGATGTCCTCAATATTAATCAATTAAGGGGTGATTAATACTACTACTATATG 1140  
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Qy 1141 CTTGCCACCAAGGAGAGTTTATACTATTTCTGGCTGGGATACCTTCACTGTAAT 1200  
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Qy 1261 GTTGATGGTTCCTGTTTGTATCTTGCAATCAATATGACAGAGGTTCCAGTCTGTGGAT 1320  
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Qy 1321 CCAGTTAACGTGTATGAGCTCCAAATAGAGGTGACATGATCAACAGGAGCACTCTT 1380  
Db 1321 CCAGTTAACGTGTATGAGCTCCAAATAGAGGTGACATGATCAACAGGAGCACTCTT 1380  
Qy 1381 GTTACTCCACATTTATGACATGATCAGCAATGACCCCAATCTTGGAGGCGTCAAGCTC 1440  
Db 1381 GTTACTCCACATTTATGACATGATCAGCAATGACCCCAATCTTGGAGGCGTCAAGCTC 1440  
Qy 1441 ATTGCTGAAGCATGGATGCAAGGCGCTCTATCAAGTAGTCAATTCCTCACTGGAAT 1500  
Db 1441 ATTGCTGAAGCATGGATGCAAGGCGCTCTATCAAGTAGTCAATTCCTCACTGGAAT 1500  
Qy 1501 GTTGGTCTGAGTGGAAATGGGAATGACGGGACATTTGTGGTCAATTCATTAAGGCAT 1560  
Db 1501 GTTGGTCTGAGTGGAAATGGGAATGACGGGACATTTGTGGTCAATTCATTAAGGCAT 1560  
Qy 1561 GATGGAATTTGCTGGTGGTTTGGCGAATGCTTTGTGGAGTCCACCTATACCGGTA 1620  
Db 1561 GATGGAATTTGCTGGTGGTTTGGCGAATGCTTTGTGGAGTCCACCTATACCGGTA 1620  
Qy 1621 AGTTGTGCAATCTTGTAAATGAGTTGAGTGAATGTCACTGGATTTTTTATATACC 1680  
Db 1621 AGTTGTGCAATCTTGTAAATGAGTTGAGTGAATGTCACTGGATTTTTTATATACC 1680  
Qy 1681 ACATGATGATACACATCTTAATAATATAAACAATCATAGTGTATGCAATTTGGCTAA 1740  
Db 1681 ACATGATGATACACATCTTAATAATATAAACAATCATAGTGTATGCAATTTGGCTAA 1740  
Qy 1741 GAAGTATTAGTGTATACACTAGTGTATATAGTTTTTAACCCCACTTGCATGAA 1800  
Db 1741 GAAGTATTAGTGTATACACTAGTGTATATAGTTTTTAACCCCACTTGCATGAA 1800  
Qy 1801 GGAAACATAGGCTTCTAGTTATCTTATTTATTTGTCGGTGAATATCCACTGAAAAAT 1860  
Db 1801 GGAAACATAGGCTTCTAGTTATCTTATTTATTTGTCGGTGAATATCCACTGAAAAAT 1860

Qy 1861 TCCAGCCATGTCAATTTTATAGGGGGAGAGAAACTATATTGATTTGCCCCCTTAAAG 1920  
Db 1861 TCCAGCCATGTCAATTTTATAGGGGGAGAGAAACTATATTGATTTGCCCCCTTAAAG 1920  
Qy 1921 AAGCCATCTCAGAAATTCATAGCTAAGTTGCTTTTCTGTAAAGAAAGAAACGACTTCAT 1980  
Db 1921 AAGCCATCTCAGAAATTCATAGCTAAGTTGCTTTTCTGTAAAGAAAGAAACGACTTCAT 1980  
Qy 1981 ACTTCTATCGGTGCTAACTTAGCTCGATGATATTTGTAAAGATGAATGCCAATTTAAT 2040  
Db 1981 ACTTCTATCGGTGCTAACTTAGCTCGATGATATTTGTAAAGATGAATGCCAATTTAAT 2040  
Qy 2041 TTGTCGGATATTTGATCTGTTATTCACAAATTTCTATTTGGTTTCTAGAAATCAAC 2100  
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Qy 2161 CTTGGCACAGTATCAACTTTGTATGTCACATGATGATTTACACTGGCTGATTTGTAA 2220  
Db 2161 CTTGGCACAGTATCAACTTTGTATGTCACATGATGATTTACACTGGCTGATTTGTAA 2220  
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Qy 2341 GGAAGAGCAGATGGCAATTTCTTGTCTCATGTTTCTCAAGGAGTTCCAATGT 2400  
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Db 2461 ATTCTTATGCTCAATTTATTTTCTGGGTAAAGAAACAACTCTCTGAGTTGCCATG 2520  
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Db 2521 TCTGCTGCTCATGACAAATTTCCGCAAGGAGTGCAGGGTCTTGGGCTTGAGGACTTTC 2580  
Qy 2581 CAAAGGCAACAGGCTGAGTGGCATGTCATCAGCTGGGAAGCTGATTTGGTCTGAGA 2640  
Db 2581 CAAAGGCAACAGGCTGAGTGGCATGTCATCAGCTGGGAAGCTGATTTGGTCTGAGA 2640  
Qy 2641 ATAGCCGATTTGTTGCTTTTCCATGAAAGATGAAAGACAGGGCGAGATCTATGTGGCT 2700  
Db 2641 ATAGCCGATTTGTTGCTTTTCCATGAAAGATGAAAGACAGGGCGAGATCTATGTGGCT 2700  
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Db 2701 TCACACACAGGCTTACCGGCTTGTAGCTCCAGAGCGCGAGGGCGGCTGGG 2760  
Qy 2761 AACCGGTGTGACACAGGCAAGCCAGCATACAGCTCTCTCAACCCACTTACCTG 2820  
Db 2761 AACCGGTGTGACACAGGCAAGCCAGCATACAGCTCTCTCAACCCACTTACCTG 2820  
Qy 2821 ATCGGCTCTCACCATAACAGTTCTCGATTTCTCTACTCCTCAACCTCTACCCCATGC 2880  
Db 2821 ATCGGCTCTCACCATAACAGTTCTCGATTTCTCTACTCCTCAACCTCTACCCCATGC 2880  
Qy 2881 TCAGTACTCATCGGTGATCTAGTTGCGGCTGATTTGAGAGACCAATATATACA 2940  
Db 2881 TCAGTACTCATCGGTGATCTAGTTGCGGCTGATTTGAGAGACCAATATATACA 2940









QY	1396	ATTGACATGATCAGCAATGACCCGATTTCTTTGGAGCGTCAAGCTCATTCGTCTGAAGCATGG	1455
DB	1484	ATTGACATGATTAGCAATGATGCCAAATTTCTTTGGAAATGTCAAGCTCATTTGCTGAAGCATGG	1543
QY	1456	GATCGAGAGCGCTCTATCAAGTAGGTCAATTCCTCAGTGGAAATGTTTCGTCTGAGTGG	1515
DB	1544	GATCGAGGAGGTCTCTATCAAGTTGGTCAGTTTCTCAGTGGAAAGCTTTGGTCAGAGTGG	1603
QY	1516	AATGGGAAGTACCGGGACATTTGGCGGTCAATTCATTAAGGCACTGATGAAATTTGCTGGT	1575
DB	1604	AATGGGAAGTATCCCGATACCGTCCGTCACTTATCAAAAGGCAAGATGATTTGCTGGT	1663
QY	1576	GGTTTTGCCAAATGCTTTCTGTGGAAGTCCACACTATACCAGTAACTAGTTCTGCGCAATACT	1635
DB	1664	GCTTTTGCTGAATGCCCTATGTGGAGTCCACAGTTATAC	1702
QY	1636	TGTAATGAGTTGAGTGAATGTCCACTGGATTTTTTTATATATACCACATGATGATACACA	1695
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QY	1696	TCTAAATATATAACATCATAGTGTATGTCATATGCATTTGCGCTAAGNAGTATTAGTGAT	1755
DB	1703	-----	1702
QY	1756	ACACTAGTCTATATATAGTGTTTTAAACCCAACTTGCCAAATGAAGGAACATAGGCGCTTT	1815
DB	1703	-----	1702
QY	1816	CTAGTTATCTTATTTATTTGTCGGTGAATTAATCCACTGAAAAATTCACGCCATGTCAATT	1875
DB	1703	-----	1702
QY	1876	TTTTAGGGGGGAGAGAAACTATATTGATTTGGCCCCCTAAAAAGAGCCATCTCAGAAT	1935
DB	1703	-----	1702
QY	1936	TCATAGTTAAGTGTCTTTTCTGTAAAGAAAGGAAACGACTTCATCTTTCTATCGGTGC	1995
DB	1703	-----	1702
QY	1996	TAACTTAGCTCGATGTATATTTGTGAAGTGAATGCCAAATTTAATTTGTCGGATAAATTG	2055
DB	1703	-----	1702
QY	2056	ATCTGTTATTCAAAAATTTCTATTTGGTTTTCTGTAGAAATCAAAACCACTAACTTGTATT	2115
DB	1703	-----	1702
QY	2116	GGCACTCCAACCTCTTATTGATTAATCAGSCAGGAGGAAGAAACCTTTGGCAGAGTATCA	2175
DB	1703	-----CAGGCAGGGGGAGGAAGCCCTTGGCAGAGTATCA	1736
QY	2176	ACTTTGTATGTGCATGATGGATTTACACTGGCTGATTTGGTAAACATATAATAAAGAAGT	2235
DB	1737	ACTTTGATGTGCACAGATGGAATTTACACTGGCTGATTTGGTCACATACAATAGCAAGT	1796
QY	2236	ACAAATTACAAATATGGGGAGAACCAACAGAGATGAGAAAAATCACAATCTTTAGCTGGAATT	2295
DB	1797	ACAACTTGTCAAAATGGTGAGACCAACAGAGATGGGAAAAATCATAAATCTTTAGCTGGAATT	1856
QY	2296	GTGGGAGGAGGAGAAATTCGACAGATTTGTCGTCAAAAGATTTCAGAGAAAGGAGGACAGATGC	2355
DB	1857	GTGGGAGGAGGAGAAATTTGCAAGTCTGTGACGCCAGATTAAGGAAGAGGCAAAATGC	1916
QY	2356	GCAATTTCTTTTGTCTCATGTTTCTCAAGAGATTCCAATGTTCTACATGGGTGATG	2415
DB	1917	GCAATTTCTTTTGTCTTATGTTTCTCAGGGAGATTCCAAATGTTCTACATGGGCGATG	1976
QY	2416	AATATGCCACACAAAAGGGGGCAACAACATACATACTGCCATGATCTTTATGTCTCAATT	2475
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QY	2476	ATTTTCTCGGATATAAAA--AAGAACAAATACTCTGAGTTGCAACCGGATCTGTGTCCTCA	2532

Db	2037	ATTTCGGTTGGGATAAAGAGGAACAAATCTCTGATTTGTACAGATTCTGGCGTCTCA	2096
Qy	2533	TGACCAAAATTCGCAAGGAGTTCGAGGGTCTTTGGCCTTTGAGACTTTTCCAAAGCCCAAC	2592
Db	2097	TGACCAAAATTCGCAAGGAATGTGAATCTCTTGGCCTTTGAGACTTTCCCGACTTCAGAAC	2156
Qy	2593	GGCTGAGTGGCATGCTCATCAGCCTGGAGAGCCTGATTTGCTCTGAGATAGCCGATTTCG	2652
Db	2157	GGTTGAAATGGCACGGTCAACAGCCCGGAGCCCTGACTTGGTCAAGCAAGCCGATTTCG	2216
Qy	2653	TTGCCCTTTTCCATGAAGAATGAAGACAGGGCGAGATCTATGTGGCCTTCAACACCAAGCC	2712
Db	2217	TTGCCCTTCAACATGAAGGACGAAACCAAGGCGAGATCTAGTGGCCTTCAACACCAAGTC	2276
Qy	2713	ACTTACGGCCGTTGTTGAGCTCCAGAGCGGACGGCGGGTGGGAAACGGTGGTGG	2772
Db	2277	ACCTTCGGTGGTGTGTTGGCTTCAGAGCGCTCTGGGTTCGATGGGAGCGGTGGTGG	2336
Qy	2773	ACACAGCAAGCCAGCACCATACGACTTCTCTCACCGAGACTTACTCTGATCGCGCTCTCA	2832
Db	2337	ACACCGCAAGGAGGACCATATGACTTCTCAACGATGGCTGCCAGATCGTCTGTCA	2396
Qy	2833	CGATACACGATTTCTCGATTTCTCTACTCCAACTCTACCCATGCTCAGCTACTCAT	2892
Db	2397	CCGTCTACCAAGTTCTCTCATTTTCCCTCAACTCTCTATCTCTCAGTACTCTCT	2456
Qy	2893	CGGTCTATCTTAGTATTGCGCCCTGATGTTTGAGAGACCAATATATA	2938
Db	2457	CCATCATCTCTGATTGCGCCCTGATGCTGAAAGACAGATACA	2502
RESULT 6			
US-10-425-114-19788			
; Sequence 19788, Application US/10425114			
; Publication No. US2004003488A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yifua			
; APPLICANT: Kovacic, David K.			
; APPLICANT: Screen, Steven E			
; APPLICANT: Tabaka, Jack E			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
; FILE REFERENCE: 38-21(53313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 19788			
; LENGTH: 1866			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; OTHER INFORMATION: Clone ID: LIB3151-045-C7_FLI			
US-10-425-114-19788			
Query Match 25.9%; Score 777; DB 13; Length 1866;			
Best Local Similarity 65.4%; Pred. No. 1.1e-200;			
Matches 1477; Conservative 0; Mismatches 250; Indels 530; Gaps 2;			
Qy	685	GGGACCTTACCTTAGATATCTTCAAAGGACCTGGTAATATATAGATGCACTTGGCT	744
Db	1	GGTGACCTACCCCTTGGGTACCATCAGAAGGACCTTGTCATATATGAATGCATTTGGCT	60
Qy	745	GGATTCAAGACATGATTCAGCAATGTAGAACAATCCGGGTACTTTTCATTGGAGCTGTG	804
Db	61	GGATTCAAGAAGACAACTCAAGCAAGACAAACCCAGGAACCTTACATTGGTCTGTG	120
Qy	805	TCGAGCTTGACTATTGTTGAGGAGCTTGAGTTAATTGTTGAATTAATGCCCTGCCAT	864
Db	121	TCAAAGCTTGACATCTAAAGGAACTTGAGTGAATGTATAGACTAATGCCCTGCCAT	180





APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIPT300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 218  
LENGTH: 2352  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-218

Query Match 22.0%; Score 658.4; DB 9; Length 2352;  
Best Local Similarity 71.2%; Pred. No. 3.3e-168;  
Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;

389 TGCTGACGATAGGTCACCGAGGAGTTCCCTTGACCCCTGATCAATCGACCGGGA 448  
323 TCCGTGAGAACAAAGTACCGAGAGAGTTCAGCTTGATCCATCAAGAAATAGAACTGGCC 382  
449 ACCTGTGGCATGCTTCATCGAAGCGAGCTGCACAAATGCTTTACGGGTACAGGTTG 508  
383 ATGTTTGGCATGCTTCATCGAAGCGAGAGTTCAGAGATATGTTGATGTTATAGATTG 442  
509 ACAGCACTTTGCTCTCACTGCGGGCACTACCTTGATGTTTCAATGTCGTGGTGATC 568  
443 ATGGCAAGTTTCTCTCGAAGAGAGTTCATTTATGATATTCCTCAACATTTTATGGATC 502  
569 CTATGCTAAGGCGATGATTAAGCGAGGAGTATGTTGTTCCAGCGGTGTAACAATT 628  
503 CTACGCAAGGCAATTTATAGCAGAGATGAGTTTGGAGTTTGGACCTGATGATTAAT 562  
629 GCTGGCTCAGATGGCTGGCATGATCCCTCTTCCATATAGACGTTTGTATGGAGAGGG 688  
563 GTTGGCTCAATGGCTGTATGATCCCACTCGTGAAGAGAGTTTGTATGGAGAGGG 622  
689 ACCTACCTTAAGATATCCTCAAGACCTGGTGAATATATAGATGACCTTCGCTGGAT 748  
623 ATATGCACTGAAGCTTCCACAGAAAGATCTTGTATATGAAATGCATGTCGAGGTT 682  
749 TCAGCAAGCATGATTTCAAGCAATGAGAACATCCGGGTACTTTCAATGGAGCTGTGTGGA 808  
683 TTCAAGGCATGAGTCTAGTAAATTTGAATTCCTGGCACATACCAGGGTGTTCAGAGA 742  
809 AGCTTGACTATTTGAAGAGCTTGGAGTTAATGTTATGTAATTAATGCCCTGCAATGAGT 868  
743 AGCTTGACCAATTTGAAGAGCTTGGGATAAATTTGATAGAATTAATGCCATGTCAGGAT 802  
869 TCAAGGAGCTGGAGTACTCAACCTCTTCTTC-----CAAGATCAACTTTT 913  
803 TTATGAGCTGGAGTATTAAGCTACATAGATTTTGGAGACCAAGGGTAAATTTT 862  
914 GGGATATTTACCAATAAATTTCTTTTCAACAATGACAAGATACATACAGCGGGGATAA 973  
863 GGGGTACTCTACCAATTTGGGTCTCTCTCGCCATGATCAGATCGCATCAGCAAGCTCTA 922  
974 AAACTGTGGCGTGGATCCCAATATGAGTTCAAACTTTTGAAGAGAGGCTCAACAAC 1033  
923 ACAATTTTGTGGAGAGGCCAATAAATGAATTTCAAAATTTCTTTTGAAGAGGCACATAAC 982  
1034 GGGGAATGAGGTGATCTGATGATTTGTTCTTCAACCATACAGCTGAGGGTAAATGAGAATG 1093  
983 GAGGAATGAGGTAATCATGATGCTGCTTTGTAACCAACACAGCGGAAGGAATGATAAAG 1042

1094 GTCCAAATATATATCAATTAAGGGGTGATATACTATATATATATGTTGACCCCAAGG 1153  
1043 GGGCCATTTTCTCATTTAGAGAGTTGATAACAGAGTGTCTATTACATGTTGCTCCAAAGG 1102  
1154 GAGAGTTTATAAATCACTATTCGCTGGTGGAAATACCTTCAACTGTAATCATCTCTGGTTC 1213  
1103 GGGAGTTCTATAATTAATTCAGGCTGTGTATAATCATCACTGCAATCATCTCTGGTTC 1162  
1214 GTCAATTCATTTGTAGATTTTAAAGATCTCGGTGACGGAATGATGATGATGATGATGATG 1273  
1163 GTCAATTCATTTGGATTCCTGAGATATTTGGTTTACAGAAATGATGTTGACGGCTTCC 1222  
1274 GTTTTGTATCTTGCATCCATATGACAGAGTTCCAGTCTGCTGGATCCAGTTAACGTTG 1333  
1223 GCTTTGATCTTTGGTTCAATCATGTCAGGACAGAGCTTTGGATCCAGCCAAATGTTT 1282  
1334 ATGGAGCTCCAAATAGAGGTGACATGATCAACAAGGACACCTCTTCTTACTCCACCAC 1393  
1283 ACGGGGCTGATGTAGAGGTGACTTGTCTCAACTGGTACTCTTATTAGTGCCTCCAG 1342  
1394 TTATGACATGATCAGCAATGACCAATTTCTTGGAGGGTCAAGCTCATCTGCTGAGCAT 1453  
1343 TAAATGACATGATAAGTAATGATCCATCTCCCGGTGTTAAGCTAATAGCTGAAGCAT 1402  
1454 GGGATGACAGGAGCTCTATCAAGTAGGTCAATTCCTCACTGGAATGTTTGGTCTGAGT 1513  
1403 GGGATGCGGGTGGCTGTACCAAGTTGGCATGTTTCCACACTGGGTATTTGGTCTGAGT 1462  
1514 GGAATGGAAAGTACCGGACATTTGCGTCAATTCATTAAGGCACTGATGATGATGATG 1573  
1463 GGAATGGAAAGTTTCCGGATGTTGTGAGACAGTTTATAAAGGACCAAGTGGCTTTCTG 1522  
1574 GTGGTTTGGCAAGTCTTTGTGGAAGTCCACACCTATACAGGTAAGTTG 1625  
1523 GTGCTTTGCTGAATGCTCTGTGAAGCCCAATCTGTACAGGAGGTAG 1574

RESULT 8

US-09-938-842A-218  
Sequence 218, Application US/09938842A  
Publication No. US20040009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIPT300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 218  
LENGTH: 2352  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-218

Query Match 22.0%; Score 658.4; DB 11; Length 2352;  
Best Local Similarity 71.2%; Pred. No. 3.3e-168;  
Matches 891; Conservative 0; Mismatches 346; Indels 15; Gaps 1;  
389 TGCTGACGATAGGTCACCGAGGAGTTCCCTTGACCCCTGATCAATCGACCGGGA 448  
323 TCCGTGAGAACAAAGTACCGAGAGAGTTCAGCTTGATCCATCAAGAAATAGAACTGGCC 382



Qy	2672	TGAAGA	CAGCGG	CGAGAT	CTAT	TGTGGCTT	CAAC	CACAGCC	CACTT	ACCGCGCT	TGTTGA	27331		
Db	745	CGAAAC	CAAAAG	GGCGAG	ATCT	ACGTGG	CGCTT	CAAC	CACAGT	CACCTT	CCGCTG	TGTTGG 804		
Qy	2732	GCCTCC	AGAGCG	CGCAG	GGCG	CCGCTG	GGAA	CCGCTG	GACAC	AGCAAG	CCAGCAG	CACC 27911		
Db	805	GCCTTC	AGAGGG	CTCT	CGGCTT	CCGAT	GGGACC	CGGTG	GTGAC	CACCGG	CAAGGAG	GGCACC 864		
Qy	2792	ATACGA	CTTCTC	ACCG	AGCA	CTTAC	CTGAT	CGCGT	CTCT	CACCA	TACAC	CAGTTCTCGCA 28511		
Db	865	ATATGA	CTTCTC	ACCG	ATGG	CGCTT	CGCAG	ATCGT	CTGT	CACCT	CTTAC	CAGTTCTCTCA 924		
Qy	2852	TTTCTC	TCTACT	CCAA	CGCTT	ACCC	ATGCT	CAGT	CTCAT	TCGCT	CACT	CCTAGTAT	TGCG 29111	
Db	925	TTTCTC	CACT	CCAA	CTTCT	TAT	CTCT	ATCT	GTCT	CAGT	CTACT	CTCTCC	ATCATCTCTG	TATGCG 984
Qy	2912	CCCTGA	TGTTG	AGAG	ACCA	TA	TATA						2938	
Db	985	CCCTGA	TGCTCT	GAA	AGAG	AGCAG	ATACA						1011	

## RESULT 10

```

US-09-850-936-1
; Sequence 1, Application US/09850936
; Publication NO. US20030167527A1
; GENERAL INFORMATION:
; APPLICANT: Emmermann, Michael
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; TITLE OF INVENTION: FROM POTATO
; FILE REFERENCE: GFB8
; CURRENT APPLICATION NUMBER: US/09/850,936
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US/09/187,124
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/EP97/02292
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: DE 196 18 125.9
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1819)
; OTHER INFORMATION: Clone: Iso5
US-09-850-936-1

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Db	241	CTGTATAGAGCTAATGCCCCTGTGCAGAGTTTCAATAGAGCTGGAGTACTATATAGTTATTAATC	300
Qy	900	-----CAAGATGAACCTTTTGGGGATATTTACCATAAACTTCTTTTCACC	944
Db	301	TGTATTGGGCGACTACAAGTTTAACTTTTGGGCTATTCTACTGTCAATTTCTTTTCTCC	360
Qy	945	AATGACAGAGATACACATCAGCGGGATAAAAACTGTGGCGGTGATGCCATAAATGAGTT	1004
Db	361	AATGGGAAGATATCTCGTCTCTTAAGTAATTTGGGCGCTCGGTGCAATAAACGAATT	420
Qy	1005	CAAAACCTTTTGTAAAGAGAGGCTCACAAACGGGGAATTTAGGTGATCTCTGATGTGTGCTT	1064
Db	421	TAAGTATCTTTGCAAGGAAGCACATAAAACGTGGAATCGAGGTTATCATGATGTGTGTTT	480
Qy	1065	CAACCATACAGCTGAGGGTAATGAGAAATGTCCTCAATATTAATCAATTTAAGGGGTGATAA	1124
Db	481	CAATCACACTGCTGAAGGAATGAAATGTCCTACTATCATATTTAGAGGCATTGACAA	540
Qy	1125	TACTACATATATATGCTTCACCAAGGAGAGTTTTATAACTATTCTGCTGTGGAA	1184
Db	541	CAGTGTGTTTATACGCTAGCTCCTAAGGTGAAATTTACAACACTCAGGATGTGGAA	600
Qy	1185	TACCTTCAACTGTAATCATCTCTGGTTCGTCAATTCATTTGTAGATTTGTTTAAAGTACTG	1244
Db	601	TACCTTCAACTGTAATTAATCCCATGTACGTCAATTTATAGTGGATGCTTTGAGATATTG	660
Qy	1245	GGTGACGGAATGCATGTTGATGTTTTGTTTTGATCTTGATCCATAATGACCAGAGG	1304
Db	661	GGTTACCGAAATGCACGTAGATGCTTCCGCTTTGATCTTGCTTCTATCCTTACAGAAG	720
Qy	1305	TTCCAGTCTGTGGATCCAGTTAACGGTGTATGAGCTCCAATAGAAGTGACATGATCAC	1364
Db	721	TAGCAGCTCGTGGAAATGCTGTAATGCTATGGAATTTCAATTTGACGTCACATGATCAC	780
Qy	1365	AACAGGACACCTCTGTTACTCCACACTTATTGACATGATCAGGAATGACCAATCT	1424
Db	781	CACAGGCACCTCTCAAGGCCACCAITTGATTTGATATGATTAGCAATGATCAATACT	840
Qy	1425	TGGAGGCGTCAAGCTCATTTCTGAAGCATGGGATGACGAGGCGCTCTATCAAGTAGGTCA	1484
Db	841	TAGTGGAGTAAAGCTTATAGCTGAAGCATGGGATTTGTGGAGGCTTTTACCAAGTTGGCAT	900
Qy	1485	ATTCCTCTACTGGAATGTTTGGTCTGAGTGGAAATGGGAAGTACGGGACATTTGGCGTCA	1544
Db	901	GTTTCCGCATCTGGGATATCTGGTCGGAGTGGAAACGGAAAGTACCGTGACATGTCAGTCA	960
Qy	1545	ATTCATTAAAGGCACATGATGGATTTGCTGGTGTGTTTCCGGAATGCTTTTGTGGGAAGTCC	1604
Db	961	GTTTCATCAAGGCATGATGGTITTTCTGGGCTTTTGCTGAATGCTTTTGTGGGAAGCC	1020
Qy	1605	ACACCTATACAGGTAAAGTTTGGCAATATCTGTAATGAGTTGAGTGAAATGTCACCTGG	1664
Db	1021	AAATCTATACGAAGAGGAGAAACCAATGGACAGTATAAAATTTCTGTTGTGGCCA	1080
Qy	1665	ATTTTATATATACCATGATGATACATCTAAATATATAAACAAATCATAGTGTATGC	1724
Db	1081	CGATGGTTTTACTTTGGCTGAATTTAGTGACATACACAAATAAACCAATTTGCGCAATGG	1140
Qy	1725	ATAATG	1729
Db	1141	AGAGG	1145

## RESULT 17

```

RES-001.11
; Sequence 6193, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E

```

APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(531313)B  
; CURRENT APPLICATION NUMBER: US/10/425.114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 6193  
; LENGTH: 1830  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700556474\_FLI  
US-10-425-114-6193

Query Match 14.0%; Score 421; DB 13; Length 1830;  
Best Local Similarity 75.9%; Pred. No. 1.9e-103;  
Matches 520; Conservative 0; Mismatches 165; Indels 0; Gaps 0;  
QY 967 GGGATAAAAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTAAAGAGGCT 1026  
DB 4 GGCATACGAACTGTGGCAGGATGGGATTAATGAAATTAATTCCTGATCAAGAGGCG 63  
QY 1027 CACAAACGGGAATGAGGTGATCCTCGATGTTCTTTCAACCATACAGCTGAGGGTAAT 1086  
DB 64 CACAAACGGAATAGAGGTATCATGATGTTGTTTCAATCATACAGCTGAGGGTAAT 123  
QY 1087 GAGATGTCCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1146  
DB 124 GAGATGTCCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 183  
QY 1147 CCCAAGGGAGAGTTTATAACTATCTTGGCTGTGGGATACCTTCAACTGATTAATCATCT 1206  
DB 184 CCCAAGGGAGAGTTTATAACTATCTTGGCTGTGGGATACCTTCAACTGATTAATCATCT 243  
QY 1207 GTGTTTCGTCATTTAGATTTGTTTAAAGATTAAGATTAAGATTAAGATTAAGATTTGAT 1266  
DB 244 GTTGTGCGACAAATTAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 303  
QY 1267 AACGTGTATGAGCTCCAAATAGAGGTGACATGATCAACAGGAGACACCTCTTGTGTACT 1386  
DB 364 AATGATTTGTTGCTCCAAATAGAGGTGACATGATCAACAGGAGACACCTCTTGTGTACT 423  
QY 1387 CCACCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1446  
DB 424 CCACCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483  
QY 1447 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 1506  
DB 484 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 543  
QY 1507 TCTGAGTGGGATGGGAAGTACCGGACATTTGGCGTCAATTCATTAAGGACATGATGGA 1566  
DB 544 TCAGAAATGGGATGGGAAGTATAGACACGCGTGGCTGTTTATCAAGGGTACAGATGGC 603  
QY 1567 TTTGCTGTGTTTGGCGAATGCTTTTGGGAGTCCACACCTATACAGGTAAGTTGT 1626  
DB 604 TTTGCTGTGTTTGGCGAATGCTTTTGGGAGTCCACACCTATACAGGTAAGTTGT 663  
QY 1627 GGCATACTTGAATGAGTTGAGT 1651  
DB 664 AGAAAACCGTCATAGTATTAATCT 688

RESULT 12

US-10-424-599-11817  
; Sequence 11817, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424.599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 11817  
; LENGTH: 2052  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_110679C.1  
US-10-424-599-11817

Query Match 14.0%; Score 421; DB 13; Length 2052;  
Best Local Similarity 75.9%; Pred. No. 2.1e-103;  
Matches 520; Conservative 0; Mismatches 165; Indels 0; Gaps 0;  
QY 967 GGGATAAAAACTGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTAAAGAGGCT 1026  
DB 4 GGCATACGAACTGTGGCAGGATGGGATTAATGAAATTAATTCCTGATCAAGAGGCG 63  
QY 1027 CACAAACGGGAATGAGGTGATCCTCGATGTTCTTTCAACCATACAGCTGAGGGTAAT 1086  
DB 64 CACAAACGGAATAGAGGTATCATGATGTTGTTTCAATCATACAGCTGAGGGTAAT 123  
QY 1087 GAGATGTCCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1146  
DB 124 GAGATGTCCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 183  
QY 1147 CCCAAGGGAGAGTTTATAACTATCTTGGCTGTGGGATACCTTCAACTGATTAATCATCT 1206  
DB 184 CCCAAGGGAGAGTTTATAACTATCTTGGCTGTGGGATACCTTCAACTGATTAATCATCT 243  
QY 1207 GTGTTTCGTCATTTAGATTTGTTTAAAGATTAAGATTAAGATTAAGATTAAGATTTGAT 1266  
DB 244 GTTGTGCGACAAATTAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 303  
QY 1267 GGTTCGTTTGTGATTTGTCATTAATGATTAAGATTAAGATTAAGATTAAGATTTGAT 1326  
DB 304 GGTTCGTTTGTGATTTGTCATTAATGATTAAGATTAAGATTAAGATTTGAT 363  
QY 1327 AACGTGTATGAGCTCCAAATAGAGGTGACATGATCAACAGGAGACACCTCTTGTGTACT 1386  
DB 364 AATGATTTGTTGCTCCAAATAGAGGTGACATGATCAACAGGAGACACCTCTTGTGTACT 423  
QY 1387 CCACCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1446  
DB 424 CCACCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483  
QY 1447 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 1506  
DB 484 GAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCTCACTGGAATGTTGG 543  
QY 1507 TCTGAGTGGGATGGGAAGTACCGGACATTTGGCGTCAATTCATTAAGGACATGATGGA 1566  
DB 544 TCAGAAATGGGATGGGAAGTATAGACACGCGTGGCTGTTTATCAAGGGTACAGATGGC 603  
QY 1567 TTTGCTGTGTTTGGCGAATGCTTTTGGGAGTCCACACCTATACAGGTAAGTTGT 1626  
DB 604 TTTGCTGTGTTTGGCGAATGCTTTTGGGAGTCCACACCTATACAGGTAAGTTGT 663  
QY 1627 GGCATACTTGAATGAGTTGAGT 1651  
DB 664 AGAAAACCGTCATAGTATTAATCT 688

RESULT 13

US-10-425-114-15962



Db 991 ATGGTGTGGACTGTCTGCGATACTGGACACGCGAATTTTCATATTGATGTTTTGCGCTTT 1050  
Qy 1279 GATCTTGCATCCATAATGACACGAGGTTCCAGTCTGCGGATCCAGTTAACGTGTATGGA 1338  
Db 1051 GATTAGCCTCTATTTTGGGAAGGGATCCCTG----- 1082  
Qy 1339 GCTCCAATAGAAGGTGACATGATCACACAGGGACACCTCTTGTTACTCCACCACCTTATT 1398  
Db 1083 -----GGGCTACCCCTTGCCCATCCCTCTTTG 1113  
Qy 1399 GACATGATCAGCAATGACCCCAATTTCTGGAGGCGTCAAGCTCATTTGCTGAAGCATGGAT 1458  
Db 1114 GAAACCCCTGGCCTTTGATCCCATTTTGGCCCGTTCCAACTTATTGCTGAAGCCTGGGAT 1173  
Qy 1459 GCAGGAGGCCCTCTATCAAGTAGGTCAATTCCTCACTGGAATGTTTGGTCTGAGTGAAT 1518  
Db 1174 GCCGTGGGCTATACCAAGTAGGATCTTTTCCAGTTATGGCCGCTGGCCGGAATGGAAT 1233  
Qy 1519 GGGAAGTACCGGACATTTGTCGTCAATTCATTAAGGCACTGATGGATTTGCTGTGGT 1578  
Db 1234 GGGAAATACCGAGATACGGTCCGAAATTTATTAAAGGAGATCGGGGGTAATTGGGGAA 1293  
Qy 1579 TTTGCCGATGCTTTTGTGGAGTCCACACTATACCAGGTA 1620  
Db 1294 ATGCCCAAGGCTACAGGGTTCCCGGACCTTTATCAAGGA 1335

## RESULT 15

US-10-425-114-7405  
; Sequence 7405, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 7405  
; LENGTH: 815  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700659189\_FLI  
US-10-425-114-7405

Query Match 6.3%; Score 187.8; DB 13; Length 815;  
Best Local Similarity 65.8%; Pred. No. 5.1e-40;  
Matches 273; Conservative 0; Mismatches 142; Indels 0; Gaps 0;  
Qy 2505 TCTGAGTGCACCGATTCTGTGCTCATGACCAAAATTCGCAAGGAGTGGAGGGTCTT 2564  
Db 3 TCAGACTTCTTCAGATTGTCGCTTATGACTAAGTTCGCGAGGAATGTGAATCGCTA 62  
Qy 2565 GGCCTTGAGGACTTTCCAAACGGCCAAACGGCTGCAGTGGCATGGTTCATCAGCTGGGAAG 2624  
Db 63 GGCCTTAGCTGACTTCCCAACCTCTGAGAGGCTGCAGTGGCATGGTTCATTTCTCGGAAAG 122  
Qy 2625 CCTGATGGTCTGAGATAGCCGATTCTGTCCTTTTCCATGAAGATGAAGACAGGGC 2684  
Db 123 CCAGACTGGTCTGAAACGAGCGTTTGTGGCTTGTATACCATGGTAGATTCAAGTGAAGGGA 182  
Qy 2685 GAGATCTATGTGGCTTTCAACACGAGCACTTACCGGCCGTTTGTGAGTCTCCAGAGCGC 2744  
Db 183 GAAATATACATTGCTTTCAATATGAGTCATTACCTTTACAGTTACCTTGGCGGAGCGT 242  
Qy 2745 GCAGGGCGCGGTGGGAACCGGTGGTGGACACAGGCAAGCCAGCATACGACTTCCTC 2804

Db 243 CCTGGATACAAATGGGAACCTCTTTGTAGACACCAAGCCTACACCATATGATTTCTCTC 302  
Qy 2805 ACCGACGACTTACCTGATCGGCTCTACCATACACAGTTCTCGCATTTCTCTACGCC 2864  
Db 303 ACTCCTGACCTTCTCTGGGAAGAGATATTGCCATACACAGTATGCTCAGTTTCTGGAGCC 362  
Qy 2865 AACCTCTACCCCATGCTCAGCTACTCATCGGTCTATCTCTAGTATTGCGCCCTGATG 2919  
Db 363 AATATGATCCCATGCTTAGTTATTCTTCATTATCTCTTGGCAATCCAGATG 417

Search completed: August 10, 2004, 01:20:08  
Job time : 1308 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2004, 14:46:38 ; Search time 7308 Seconds  
(without alignments)  
12246.436 Million cell updates/sec

Title: US-09-674-817B-2

Perfect score: 2997

Sequence: 1 ggtcggcgccggcgccgcg.....aaaaaaaaaaaaaaaaaaaaa 2997

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_lman:*
23: em_gss_lmus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	623.2	20.8	910	13	BQ609719
2	581.8	19.7	737	13	BQ609582
3	580.4	19.7	625	14	CD897285
4	565.4	18.9	617	13	BU997255

5	556.6	18.6	590	12	BJ267405
6	525.4	17.5	578	10	B8493792
7	498.2	16.6	536	13	BU971724
8	485.4	16.2	519	13	BU970613
9	479.4	16.0	508	14	CD890597
c 10	468.4	15.6	564	12	BJ272361
11	452.4	15.1	697	14	CA199345
12	431.2	14.4	622	14	CF041929
13	414.2	13.8	445	13	BU974414
14	408.4	13.6	438	13	BU971179
15	407.6	13.6	438	13	BU971450
c 16	407	13.6	591	14	CB605134
c 17	405.6	13.5	584	14	CB877804
c 18	403.8	13.5	474	14	CD890598
c 19	396	13.2	644	9	AI737641
c 20	393.2	13.1	551	14	CB617184
c 21	390.2	13.0	913	12	B8444934
c 22	390	13.0	435	10	B8425551
c 23	379.2	12.7	475	13	BQ167195
c 24	379.2	12.7	477	13	BQ609691
c 25	378.4	12.6	753	13	BQ865760
c 26	366.2	12.2	479	14	CB858538
27	350	11.7	431	12	BM500514
28	346	11.5	561	13	BU933907
29	342.2	11.4	423	13	BU974906
30	328	10.9	469	12	BI075394
31	324.4	10.8	496	14	CF040681
32	319.6	10.7	655	14	CB035933
c 33	319	10.6	574	9	AI901664
34	315	10.5	497	14	CD442761
35	314.6	10.5	582	13	BU043560
c 36	311	10.4	675	13	CA109043
37	305.6	10.2	592	12	BI934640
38	303.2	10.1	580	12	BI934559
c 39	291.4	9.7	785	12	BJ591026
c 40	285.2	9.5	473	14	CK101133
41	278.6	9.3	558	10	AW832588
42	271.8	9.1	547	12	EM178903
c 43	270.8	9.0	781	14	CD576563
c 44	270.6	9.0	729	12	BU595165
c 45	263.4	8.8	669	14	CD003812

#### ALIGNMENTS

#### RESULT 1

BQ609719/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BQ609719 910 bp mRNA linear EST 25-JUN-2002  
BRY 5805 wheat EST endosperm library Triticum aestivum cDNA 5',  
mRNA sequence.  
BQ609719  
BQ609719.1 GI:21559058  
EST.  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poaceae; Triticaceae; Triticum.  
1 (bases 1 to 910)  
Clarke,B., Lambrecht,M. and Rhee,S.Y.  
Arabidopsis genomic information for interpreting wheat EST  
sequences  
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
22478026  
12590341  
Contact: Lambrecht M.  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@acoma.stanford.edu.

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BRY 5805 wheat EST endosperm library Triticum aestivum cDNA 5',  
mRNA sequence.  
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BQ609719.1 GI:21559058  
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Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poaceae; Triticaceae; Triticum.  
1 (bases 1 to 910)  
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Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@acoma.stanford.edu.

```

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        /cultivar="Wyuana"
        /db_xref="taxon:4565"
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  Db 720 GGGTTCACAGGAGGTCCCTTGACCCCTGATGATCGGACGCGGGGAAGGTGTGGCAT 661
  QY 460 GTCTT-CATCAAGCGAGCTGCACACATGCTTTACGGGTACAGGTTCCAGCGCACCTT 518
  Db 660 GTTTTCATGGAAGCGAAGCTGCACACATACCTTAACGGGAACAGGTTCCAGCGCGCTTT 601
  QY 519 TGCTCTCACTGCGGCACTACCTTGATGTTTCCAAATGTC-GTGGTGGATCCTTATGCTA 577
  Db 600 TGTCTCTCACTGCGGCACTACCTTGATGTTTCCAAATGTCGTTGGTGGATCCTTATGCTA 541
  QY 578 AGGCAGTGATTAAGCGGAGGGG-AGTATGGTGTCCAGCGGTGGTACAAATTCCTGSCCT 636
  Db 540 AGGCAGTGATTAAGCGGAGGGAAGTATGGTGTCCAGCGGTGGTACAAATTCCTGSCCT 481
  QY 637 C-AGATGGCTGGCATGATCCCTCTTCCATATAGCACGTTTTCATTTGGGAAGCGACCTACC 695
  Db 480 CAAGATGGCTGGCATGATCCCTCTTCCATATAGCACGTTTTCATTTGGGAAGCGACCTACC 421
  QY 696 TCTAAGATATCCTCAAAAGACCTGGTAAATATATAGATGCATTCGGTGGATTCAGAA 755
  Db 420 TCTAAGATATCCTCAAAAGACCTGGTAAATATATAGATGCATTCGGTGGATTCAGAA 361
  QY 756 GCATGATTCAGCAATGTAGAACATCCGGGTACTTTTCATTTGGAGCTGTGTGCAAGCTTGA 815
  Db 360 GCATGATTCAGCAATGTAGAACATCCGGGTACTTTTCATTTGGAGCTGTGTGCAAGCTTGA 301
  QY 816 CTATTTGAAGAGCTTGAGTTAATTGTATGTAATTAATGCCCTGCCATGAGTTCAACGA 875
  Db 300 CTATTTGAAGAGCTTGAGTTAATTGTATGTAATTAATGCCCTGCCATGAGTTCAACGA 241
  QY 876 GCTGGGTACTCAACCTCTTCTTCCAGATGAACCTTTTGGGGATATTTCTACCAATAACTT 935
  Db 240 GCTGGGTACTCAACCTCTTCTTCCAGATGAACCTTTTGGGGATATTTCTACCAATAACTT 181
  QY 936 CTTTTTCAACATGACAAGATACACATCAGCGGGATAAATAAAGCTGTGGCGTGAATGCCAT 995
  Db 180 CTTTTTCAACATGACAAGATACACATCAGCGGGATAAATAAAGCTGTGGCGTGAATGCCAT 121
  QY 996 AAATGAGTTCAAACTTTTGTAGAGAGGCTCAAAACGGGGATTCAGGTGATCCTGGA 1055
  Db 120 AAATGAGTTCAAACTTTTGTAGAGAGGCTCAAAACGGGGATTCAGGTGATCCTGGA 61
  QY 1056 TGTGTCTTCAACCATACAGCTGAGGGTAAATGAGAAATGGTCCCAATATTTATCAATTAAGGG 1115
  Db 60 TGTGTCTTCAACCATACAGCTGAGGGTAAATGAGAAATGGTCCCAATATTTATCAATTAAGGG 1

RESULT 2
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LOCUS
DEFINITION BRY 5559 wheat EST endosperm library Triticum aestivum cDNA 5',
            mRNA sequence.
ACCESSION BQ609582
VERSION BQ609582.1 GI:21558921
KEYWORDS EST.

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SOURCE
  ORGANISM
    Triticum aestivum (bread wheat)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooidae; Triticeae; Triticum.
  REFERENCE
    1 (bases 1 to 737)
    Clarke,B., Lambrecht,M. and Rhee,S.Y.
    Arabidopsis genomic information for interpreting wheat EST
    sequences
  JOURNAL
    Funct.Integr. Genomics 3 (1-2), 33-38 (2003)
  MEDLINE
    22478026
  PUBMED
    12590341
  COMMENT
    Contact: Lambrecht M
    The Arabidopsis Information Resource
    Carnegie Institution of Washington, Dept. of Plant Biology
    260 Panama Street, Stanford, CA 94305, USA
    Tel: 1 650 325 1521 x 251
    Fax: 1 650 325 3748
    Email: rhee@acoma.stanford.edu.
  FEATURES
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        /organism="Triticum aestivum"
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        /cultivar="Wyuana"
        /db_xref="taxon:4565"
        /tissue_type="endosperm"
        /dev_stage="developing endosperm tissue 8, 10 and 12 DPA"
        /days_post_anthesis="1"
        /clone_lib="wheat EST endosperm library"
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    Matches 625; Conservative 0; Mismatches 17; Indels 3; Gaps 2;
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    Db 1 TAAAAAATCTGTGGCGTGATGCCATAATGATTTCAAACTTTTGTAAAGAGGCTCACA 60
    QY 1031 AACGGGAATTTAGGTGATCCTGATGTTGTCTTCAACCATACAGCTGAGGTAATGAGA 1090
    Db 61 AACGGGAATTTAGGTGATCCTGATGTTGTCTTCAACCATACAGCTGAGGTAATGAGA 120
    QY 1091 ATGTTCCAAATATTCATTTAAGGGGTGCGATATCTACATATATATGCTTCCACCCA 1150
    Db 121 ATGTTCCAAATATTCATTTAAGGGGTGCGATATCTACATATATATGCTTCCACCCA 180
    QY 1151 AGGAGAGTTTTATAAATCTTCTGGCTGTGGGAATACCTTCAACTGTAATCATCTGTGG 1210
    Db 181 AGGAGAGTTTTATAAATCTTCTGGCTGTGGGAATACCTTCAACTGTAATCATCTGTGG 240
    QY 1211 TTCGTCAATTCATGTAGATGTTTAAAGTACTGGGTGACGGAATGCAATGTTGATGGTT 1270
    Db 241 TTCGTCAATTCATGTAGATGTTTAAAGTACTGGGTGATGGAATGCAATGTTGATGGTT 300
    QY 1271 TTCGTTTTGATCTTGATCCCATTAATGACAGAGGTTCCAGTCTGTGGATCCAGTTAACG 1330
    Db 301 TTCGTTTTGATCTTGATCCCATTAATGACAGAGGTTCCAGTCTGTGGATCCAGTTAACG 360
    QY 1331 TGTATGGAGCTCCAAATAGAAAGTGACATGATCACAACAGGAGACCTCTTGTACTCCAC 1390
    Db 361 TGTATGGAGCTCCAAATAGAAAGTGACATGATCACAACAGGAGACCTCTTGTACTCCAC 420
    QY 1391 CACTTATTGACATGATCAGCAATGACCCAAATTTCTTGGAGGGCTCAAGCTCAATCTGAAG 1450
    Db 421 CACTTATTGACATGATCAGCAATGACCCAAATTTCTTGGAGGGCTCAAGCTCAATCTGAAG 480
    QY 1451 CATGGGATCGAGGAGGCTCTATCAAGTAGTCAATTCCTTCATCTGGAATGTTGGTCTG 1510
    Db 481 CATGGGATCGAGGAGGCTCTATCAAGTAGTCAATTCCTTCATCTGGAATGTTGGTCTG 540
    QY 1511 ACTGGAATGGGAAGTACCGGACATTTGCGTCAATTCATTAAAGGCACTGAT-GGATTT 1569

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Db 541 AGTGAATGGAGATACCGGACATTTGTCGCGCAATTTCTTAAGGCACTGGTGGGATTT 600
QY 1570 GCTGGTGGTTTTCGGAATG--TCTTTGTGGAAGTCCACACCTAT 1612
Db 601 GTTGGTGGTTTTCGCGAAGTCTTTTGTGAAGTCCACACCTAT 645

RESULT 3
CD897205 625 bp mRNA linear EST 14-JUL-2003
LOCUS G174.105C12F010823 G174 Triticum aestivum cDNA clone G174105C12,
DEFINITION mRNA sequence.
ACCESSION CD897205
VERSION CD897205.1 GI:32671533
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE 1 (bases 1 to 625)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
JOURNAL Poideae; Triticeae; Triticum.
COMMENT Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).

FEATURES
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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G174105C12"
/tissue_type="grain (174 degrees per day after
pollination)"
/clone_lib="G174"

ORIGIN
Query Match 19.7%; Score 590.4; DB 14; Length 625;
Best Local Similarity 99.5%; Pred. No. 8.4e-62;
Matches 613; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 2258 CAACAGAGATGGAGAAATCACAATCTTAGCTGGAATTGTGGGAGGAGGAAATTCGC 2317
Db 12 CAACAGAGATGGAGAAATCACAATCTTAGCTGGAATTGTGGGAGGAGGAAATTCGC 71
QY 2318 AAGATTCTCTCAAAAGATTGAGGAGGAGGAGATGCGCAATTTCTTTGTTCTCAT 2377
Db 72 AAGATTCTCTCAAAAGATTGAGGAGGAGGAGATGCGCAATTTCTTTGTTCTCAT 131
QY 2378 GGTTCCTCAGGAGTCCAAATGTTCTACATGGGTGATGAATATATGCGGCACACAAAAGGGG 2437
Db 132 GGTTCCTCAGGAGTCCAAATGTTCTACATGGGTGATGAATATATGCGGCACACAAAAGGGG 191
QY 2438 CAACAAATACATACACTGCCATGATTTCTATGCAATTTTTCGCTGGGATATAAAGA 2497
Db 192 CAACAAATACATACACTGCCATGATTTCTATGCAATTTTTCGCTGGGATATAAAGA 251
QY 2498 ACAATCTCTGAGTTGACCGCATTTCTGCTGCTCATGACCAAAATTCGCAAGAGTGCGA 2557
Db 252 ACAATCTCTGAGTTGACCGCATTTCTGCTGCTCATGACCAAAATTCGCAAGAGTGCGA 311
QY 2558 GGGTCTTGGCCTTGAGGACTTTCCACGGCCAAACGGCTGAGTGGCATGGTCATCAGCC 2617
Db 312 GGGTCTTGGCCTTGAGGACTTTCCACGGCCAAACGGCTGAGTGGCATGGTCATCAGCC 371
QY 2618 TGGGAGGCTGATTTGGTCTGAGATAGCCGATTCGTCCTTTTCCATGAAGTGAAG 2677
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Db 372 TGGGAAGCCTGATTTGCTGGAATAGCCGATTCGTTCCATTCGAAGATGAAG 431
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Db 432 ACAGGCGGAGATCTATGTGGCCTTCAACACAGCCACTTACCGGCGGTGTGTAGCTCCC 491
QY 2738 AGAGCGCGAGGCGCGCGTGGGAACCGGTGGTGACACAGCAAGCCAGCACCATAGA 2797
Db 492 AGAGCGCGAGGCGCGCGTGGGAACCGGTGGTGACACAGCAAGCCAGCACCATAGA 551
QY 2798 CTTCTCTACCGAGCATTTACCTGATCGCGCTCTACCATACACAGTGTCTGCAATTCCT 2857
Db 552 CTTCTCTACCGAGCATTTA-CTGATCGCGCTCTACCATACACAGTGTCTGCA-TTCTCT 609
QY 2858 CTACTCCAAACCTCTAC 2873
Db 610 CTATCCAAACCTCTAC 625

RESULT 4
BU997255 617 bp mRNA linear EST 23-OCT-2002
LOCUS HI07G18: HI Hordeum vulgare subsp. vulgare cDNA clone HI07G18
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BU997255
VERSION BU997255.1 GI:24274238
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
JOURNAL Poideae; Triticeae; Hordeum.
COMMENT 1 (bases 1 to 617)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@pk-gatersleben.de
Insert Length: 617 Std Error: 0.00
Plate: 7 row: G column: 18
Seq primer: M13rev.
Location/Qualifiers
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/db_xref="GABI:251119"
/db_xref="taxon:112509"
/clone="HI07G18"
/tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lib="HI"
/vector="pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artifact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

FEATURES
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/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lib="HI"
/vector="pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artifact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

ORIGIN
Query Match 18.9%; Score 565.4; DB 13; Length 617;
Best Local Similarity 95.7%; Pred. No. 8.6e-59;
Matches 581; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Db 11 CTTGACCCCTGATGAATCGGACCTGGGACGCTGTGGCATGTCTTCTCGTGGGAGCTG 70
QY 481 CACAACATGCTTTAGCGGTACAGGTTGCAAGGACCTTTCCTCTCTACTCGGGGCACTAC 540
Db 71 CACGECATGCTTTATGGGTACAGGTTGCAAGGACCTTTCCTCTCTACTCGGGGCACTAC 130
QY 541 CTTGATGTTTCCAAATGCTGCTGCATCCTTATCTTAAGCAGTGAATAAGCCAGGGGAG 600
Db 131 TTTGATGTTTCCAAATGTTGGTGGATCCTTATCTTAAGCAGTGAATAAGCCAGGGGAG 190
QY 601 TATGGTGTTCAGCGGCTGTGTAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTT 660
Db 191 TATGGTGTTCAGCGGCTGTGTAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTT 250
QY 661 CCATATAGCAGTTTGAATGGGAAGGCGACCTCTCTTAAGATATCTCAAAAGGACCTG 720
Db 251 CCATATAGCAGTTTGAATGGGAAGGCGACCTCTCTTAAGATATCTCAAAAGGACCTT 310
QY 721 GTAATATAGATGCACTTTCGCTGGATTCAGGAAGCATGATTCAGCAATGTAGAACAT 780
Db 311 GTAATATAGATGCACTTTCGCTGGATTCAGGAAGCATGATTCAGCAATGTAGAACAT 370
QY 781 CCGGTACTTTCATGGAGCTGTGCGAAGCTTGACTATTGGAAGGCTTGGAGTTAAT 840
Db 371 CCGGTACTTTCATGGAGCTGTGCGAAGCTTGACTATTGGAAGGCTTGGAGTTAAT 430
QY 841 TGTATTGAATTAATGCCCTGTCATGAGTTCAGGAGCTGGAGTACTCAACCTCTCTTCTCC 900
Db 431 TGTATTGAATTAATGCCCTGTCATGAGTTCAGGAGCTGGAGTACTCAACCTCTCTTCTCC 490
QY 901 AAGATGAACCTTTGGGATATCTACCAATAAATCTTTTTCACCAATGACAAATACACA 960
Db 491 AAGATGAACCTTTGGGATATCTACCAATAAATCTTTTTCACCAATGACAAATACACG 550
QY 961 TCAGCGGGATAAAAACTGTGGCGGTGATGCCATAATGAGTTCAAACTTTTGTGAAGA 1020
Db 551 TCAGGTGGATAAAAACTGTGGCGGTGATGGGATGAACAGGTTCAAACTTTTGTGAAGA 610
QY 1021 GAGGCTC 1027
Db 611 GAGGCTC 617

RESULT 5
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LOCUS
DEFINITION BU267405 Y. Ogihara unpublished cDNA library, wh_oh linear EST 09-APR-2002
aestivum cDNA clone wholif13 5', mRNA sequence.
ACCESSION BU267405
VERSION BU267405.1 GI:20087755
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 590)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 590
/organism="Triticum aestivum"

FEATURES
source

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ORIGIN

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QY 2315 CGCAGATTTGCTGTCAAAAGATTGAGGAAGGAGATCGCAATTTCTTTGTTGTCT 2374
Db 62 CGCAGATTTGCTGTCAAAAGATTGAGGAAGGAGATCGCAATTTCTTTGTTGTCT 121
QY 2375 CATGTTTTCTCAAGAGATTCCAATGTTCTACATGGGTGATGAATATGCCCACACAAAAG 2434
Db 122 CATGTTTTCTCAAGAGATTCCAATGTTCTATATGGCGATGAGTATGGCCACACAAAAG 181
QY 2435 GGGCAACAACTACATATGCTGCTGCTCATGATTTCTATGTCATTTTTCGCTGGGATAAAA 2494
Db 182 GGGCAACAACTACATATGCTGCTGCTCATGATTTCTATGTCATTTTTCGCTGGGATAAAA 241
QY 2495 AGAACAACTACTCTGAGTTGCACTGCTGCTCATGATTTCTATGTCATTTTTCGCTGGGATAAAA 2554
Db 242 AGAACAACTACTCTGAGTTGCACTGCTGCTCATGATTTCTATGTCATTTTTCGCTGGGATAAAA 301
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Db 302 CGAGGCTCTTGGCTTGGAGGACTTTCACCGGCAACGGCTGAGTGGCATGTCATCA 361
QY 2615 GCTCGGGAAGCTGATTTGCTGAGATAGCCGATTTGCTGCTTTTCCATGAAGATGA 2674
Db 362 GCTCGGGAAGCTGATTTGCTGAGATAGCCGATTTGCTGCTTTTCCATGAAGATGA 421
QY 2675 AAGACAGGCGAGATCTATGTCGCTTCAACACGAGCACTTACCGCGCTGTTGAGCT 2734
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QY 2735 CCCAGAGCGCGAGCGGCGCTGGACCGCTGTGGACACGAGCAAGCCAGCACCATA 2794
Db 482 CCCAGAGCGCGAGCGGCGCTGGACCGCTGTGGACACGAGCAAGCCAGCACCATA 541
QY 2795 CGACTTCTCCACGAGCACTTACCTGATCGGCTCTCACCATACACCAG 2843
Db 542 CGACTTCTCCACGAGCACTTACCTGATCGGCTCTCACCATACACCAG 590

RESULT 6
BU493792
LOCUS
DEFINITION BU493792 WHE1275_E05 I092S Secale cereale anther cDNA library Secale cereale
cDNA clone WHE1275_E05_I09, mRNA sequence.
ACCESSION BU493792
VERSION BU493792.1 GI:9660385
KEYWORDS EST.
SOURCE Secale cereale (rye)
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Secale.
1 (bases 1 to 578)
Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J.,
Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y.,
Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and
Tong, J.C.
The structure and function of the expressed portion of the wheat

TITLE

```

genomes - Anther cDNA library from rye  
 Unpublished (2000)  
 Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105959773  
 Fax: 5105959818  
 Email: andersowp.usda.gov  
 Sequence have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 Seq primer: Stratagene SK primer.

## FEATURES

Location/Qualifiers  
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 /organism="Secale cereale"  
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 /clone\_lib="Secale cereale anther cDNA library"  
 /note="Vector: lambda Uni-ZAP XR, excised phagemid;  
 Site 1: EcoRI; Site 2: XhoI; Plants were grown in the  
 greenhouse. Anthers were harvested and pooled from early  
 meiosis to late meiosis. The tissue, total RNA, and  
 poly(A) RNA were prepared (Butler, Ross and Gustafson) at  
 University of Missouri, Columbia. A cDNA library was  
 made, and the cDNA clones were in vivo excised to give  
 pBluescript phagemids in the TJ Close lab (Choi, Close,  
 Fenton) at the University of California, Riverside.  
 Plasmid DNA preparations and DNA sequencing were performed  
 in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 17.5%; Score 525.4; DB 10; Length 578;  
 Best Local Similarity 95.3%; Pred. No. 5.6e-54;  
 Matches 552; Conservative 0; Mismatches 26; Indels 1; Gaps 1;  
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 QY 2311 AATTGCGAAGATTTCTGTCAAAAGATTGAGGAGAGCGAGATCGCGCAATTTCTTTGTTT 2370  
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 QY 2371 GTCTCATGTTTCTCAAGGAGTCCAAATGTTCTACATGGGTGATGAATATGGCCACAA 2430  
 Db 120 GTCTCATGTTTCTCAAGGAGTCCAAATGTTCTACATGGGCGATGAATATGGCCACAA 179  
 QY 2431 AAGGGGCAACAAATACATCTGCCATGATTTCTATGTCAATTTTTCGCTGGGATA 2490  
 Db 180 AAGGGGCAACAAATACATCTGTCATGATTTCTATGTCAATTTTTCGCTGGGATA 239  
 QY 2491 AAAAAGAACAAATCTCTGAGTTGCACCGATTTCTGCTCCCTCATGACCAAAATTCGCAAGG 2550  
 Db 240 AAAAAGAACAAATCTCTGAGTTGTACCGATTTCTGCTCCCTCATGACCAAAATTCGCAAGG 299  
 QY 2551 AGTCGAGGTTTGGCTTGGAGACTTTCACAGGCGCAACGCTGCAGTCGATGGTC 2610  
 Db 300 AGTCGAGGTTTGGCTTGGAGACTTTCACAGGCTGACGCTTGCAGTGGCATGGTC 359  
 QY 2611 ATCAGCTGGGAAGCCCTGATTTGTTCTGAGAAATAGCCGATTCGTTGCCCTTTTCCATGAAAG 2670  
 Db 360 ATCAGCTGGGAAGCCCTGATTTGTTCTGAGAAAGCCGATTCGTTGCCCTTTTCCATGAAAG 419  
 QY 2671 ATGAAACAGGGCGAGATCTATGTGCTTCAACACAGCCACTTACCGGCGTTGTTG 2730  
 Db 420 ATGAAACAAAGGTGAGATCTATGTGCTTCAACACAGCCACTTACCGGCGTTGTTG 479  
 QY 2731 AGCTCCACAGCGCGGCGCGGTGGGAAACCGGTGGTGGACACAGGCAAGCCAGCAC 2790

Db 480 AACTCCAGAGCGACAGGGACCGGTGGTGGACACAGAAAGGAGCAC 539  
 QY 2791 CATACGACTTCTCACCAGCAGCTTACCTGATCGGCTC 2829  
 Db 540 CATATGACTTCTCACCAGCAGCTTACCTGATCGGCTC 578  
 RESULT 7  
 BU9711724 536 bp mRNA linear EST 22-OCT-2002  
 LOCUS HB19H15 BC Hordeum vulgare subsp. vulgare cDNA clone HB19H15  
 DEFINITION 5-3PIME mRNA sequence.  
 ACCESSION BU9711724  
 VERSION BU9711724  
 SOURCE EST.  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Hordeum.  
 REFERENCE 1 (bases 1 to 536)  
 Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.  
 Barley ESTs from developing seeds  
 Unpublished (2002)  
 COMMENT Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 Tel: 039482-5522  
 Fax: 039482-5595  
 Email: stein@ipk-gatersleben.de  
 Insert Length: 536 Std Error: 0.00  
 Plate: 19 row: H column: 15  
 Seq primer: M13rev.  
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 Location/Qualifiers  
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 /clone="HB19H15"  
 /tissue\_type="developing caryopsis"  
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 /lab\_host="XL10-Gold"  
 /clone\_lib="BC"  
 /note="Vector: pBluescript SK+; Site\_1: EcoRI (5'-end of  
 cDNA); Site\_2: XhoI (3'-end of cDNA); developing  
 caryopsis, 8-15 DAP(days after pollination) Due to a  
 cloning artefact caused by the kit, in most cases the  
 EcoRI site is NOT present, as well as the EcoRI adapter  
 used for cloning. To excise the insert, restriction sites  
 upstream EcoRI should be used (e.g. BamHI, SalI, PstI).  
 NOTE: Also due to the cloning system used Blue/white  
 selection for recombinants is not 100% reliable."  
 ORIGIN  
 Query Match 16.6%; Score 498.2; DB 13; Length 536;  
 Best Local Similarity 96.6%; Pred. No. 1.1e-50;  
 Matches 509; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 503 GTTTCGACGGCACCTTCTCTACTCGGGCACTACCTGATTTTCCAATGTCGTGG 562  
 Db 10 GTTTCGACGGCACCTTCTCTACTCGGGCACTACTTTGATGTTTCCAATGTTGTGG 69  
 QY 563 TGTATCTTATGCTAAGCAGTGATAAGCCGAGGATGATGTTTCCAGCGGTGTA 622  
 Db 70 TGTATCTTATGCTAAGCAGTGATAAGCCGAGGATGATGTTTCCGCGCATGTA 129  
 QY 623 ACAATTGTCGCTCAGATGGCTGCATGATCCCTCTTCCATATAGCAGTTTGAATGGG 682

130 ACAAATGCTGCTCAGATGGCTGGCATGATCCCTCTTCCATATAGCACGCTTTGATTGGG 189  
 683 AAGCGGACCTACCTCTAAGATATCCCTCAAAAGGACCTGGTAATATATATAGATGACCTTGC 742  
 190 AAGCGGACCTACCTCTAAGATATCCCTCAAAAGGACCTGGTAATATATATAGATGACCTTGC 249  
 743 GTGATTCACGAACATGATTCAGCAATCTAGCAATCTAGCAATCTAGCAATCTAGCAATCTAG 802  
 250 GTGATTCACGAACATGATTCAGCAATCTAGCAATCTAGCAATCTAGCAATCTAGCAATCTAG 309  
 803 TGTGCAAGCTTGACTATTGAGAGAGCTTGGAGTTAATGTTATGTTAATGTTAATGTTAATGTT 862  
 310 TGTGCAAGCTTGACTATTGAGAGAGCTTGGAGTTAATGTTAATGTTAATGTTAATGTTAATGTT 369  
 863 ATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCCAAGATGAACCTTTTGGGGATATT 922  
 370 ATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCCAAGATGAACCTTTTGGGGATATT 429  
 923 CTACCAATAAATCTTTTCCCAAGATGAACCTTTTCCCAAGATGAACCTTTTCCCAAGATGAAC 982  
 430 CTACCAATAAATCTTTTCCCAAGATGAACCTTTTCCCAAGATGAACCTTTTCCCAAGATGAAC 489  
 983 GGCCTGATGTCATTAATGAGTCTCAAACTTTTCTTGAAGAGAGGCTCAC 1029  
 490 GGCCTGATGTCATTAATGAGTCTCAAACTTTTCTTGAAGAGAGGCTCAC 536

RESULT 8  
 BU970613  
 LOCUS  
 DEFINITION HB15C17: BC Hordeum vulgare subsp. vulgare cDNA clone HB15C17  
 5-PRIME, mRNA sequence.  
 BU970613  
 BU970613.1 GI:24221406  
 EST.  
 SOURCE  
 ORGANISM  
 Hordeum vulgare subsp. vulgare  
 Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 1 (bases 1 to 519)  
 RACHUK, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.  
 Barley ESTs from developing seeds  
 Unpublished (2002)  
 Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 Tel: 039482-5522  
 Fax: 039482-5595  
 Email: stein@ipk-gatersleben.de  
 Insert Length: 519 Std Error: 0.00  
 Plate: 15 row: C column: 17  
 Seq primer: M13rev.  
 Location/Qualifiers  
 1. 519  
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 /clone="HB15C17"  
 /tissue\_type="developing caryopsis"  
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 /lab\_host="X110-Gold"  
 /clone\_lib="BC"  
 /note="vector: pBluescript SK-; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP (days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites

upstream EcoRI should be used (e.g. BamHI, SalI, PstI).  
 NOTE: Also due to the cloning system used blue/white selection for recombinants is not 100% reliable."

Query Match 16.2%; Score 485.4; DB 13; Length 519;  
 Best Local Similarity 96.9%; Pred. No. 3.8e-49;  
 Matches 495; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

ORIGIN

802 GTGTCGAGCTTGACTATTGAGAGAGCTTGGAGTTAATGTTAATGTTAATGTTAATGTTAATGTT 861  
 Db 9 GGTTCGAAGCTTGACTATTGAGAGAGCTTGGAGTTAATGTTAATGTTAATGTTAATGTTAATGTT 68  
 862 CATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCCAAGATGAACCTTTTGGGGATATT 921  
 Db 69 CATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCCAAGATGAACCTTTTGGGGATATT 128  
 922 TCTACCAATAAATCTTTTCCCAAGATGAACCTTTTCCCAAGATGAACCTTTTCCCAAGATGAAC 981  
 Db 129 TCTACCAATAAATCTTTTCCCAAGATGAACCTTTTCCCAAGATGAACCTTTTCCCAAGATGAAC 188  
 982 GGCCTGATGTCATTAATGAGTCTCAAACTTTTCTTGAAGAGAGGCTCACAAACCGGGGAATT 1041  
 Db 189 GGCCTGATGTCATTAATGAGTCTCAAACTTTTCTTGAAGAGAGGCTCACAAACCGGGGAATT 248  
 1042 GAGGTGATCTGGAGTGTGTTCTTCAACCATACAGCTGAGGTAATGAGATGGTCCAAATA 1101  
 Db 249 GAGGTGATCTGGAGTGTGTTCTTCAACCATACAGCTGAGGTAATGAGATGGTCCGAGATA 308  
 1102 TTATCATTTAAGGGGTCGATAAATGAGTCTTCACTATATATGCTTGCCACCAAGGGAGAGTTT 1161  
 Db 309 TTATCATTTAAGGGGTCGATAAATGAGTCTTCACTATATATGCTTGCCACCAAGGGAGAGTTT 368  
 1162 TATAACTATTCTGCTGCGGTAATGAGTCTTCACTATATATGCTTGCTGGTTCGTCAAATTC 1221  
 Db 369 TATAACTATTCTGCTGCGGTAATGAGTCTTCACTATATATGCTTGCTGGTTCGTCAAATTC 428  
 1222 ATTGTAGATTTTGAAGTACTGGGTGAGCGGAATGAGTGTGATGTTTTCGTTTTCGTTTTCGAT 1281  
 Db 429 ATTGTAGATTTTGAAGTACTGGGTGAGCGGAATGAGTGTGATGTTTTCGTTTTCGTTTTCGAT 488  
 1282 CTTCATCCATAATGACCAAGAGGTTCCAGTC 1312  
 Db 489 CTTCATCCATAATGACCAAGAGGTTCCAGTC 519

CD890597 508 bp mRNA linear EST 14-JUL-2003  
 G118.115A13F010718 G118 Triticum aestivum cDNA clone G118115A13,  
 mRNA sequence.  
 CD890597.1 GI:32660056  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Triticum aestivum (bread wheat)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 508)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 JOURNAL  
 COMMENT  
 Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
 and <http://genoplante-info.infobiogen.fr>).  
 Location/Qualifiers  
 1. 508  
 source

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/clone\_lib="G118"

## ORIGIN

Query Match 16.0%; Score 479.4; DB 14; Length 508;  
Best Local Similarity 97.8%; Pred. No. 2e-48;  
Matches 486; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 443 CCGGACGCTGTGCATGCTTTCATCAAGCGAGCTGCACACATGCTTTACGGGTACA 502  
Db |  
12 CTGGGAACGATGGCATGTCTTCATCAAGCGAGCTGCAGGACATGCTTTACGGGTACA 71  
QY 503 GGTTCGAGCGGCACCTTTGCTCCTCACCTGCGGCGACTACCTTGATGTTTCCAAATGTCGTGG 562  
Db |  
72 GGTTCGAGCGGCACCTTTGCTCCTCACCTGCGGCGACTACCTTGATGTTTCCAAATGTCGTGG 131  
QY 563 TGGATCCTTATGTAAGCGAGTGTATAGCCGAGGGAGTATGGTGTCCAGCGCGTGGTA 622  
Db |  
132 TGGATCCTTATGTAAGCGAGTGTATAGCCGAGGGAGTATGGTGTCCAGCGCGTGGTA 191  
QY 623 ACAATTCGTGCGCTCAGATGCGCATGATCCCTCTTCCATATAGCACGTTTGGTGG 682  
Db |  
192 ACAATTCGTGCGCTCAGATGCGCATGATCCCTCTTCCATATAGCACGTTTGGTGG 251  
QY 683 AAGCGACCTACCTCTTAAGTATATCCTCAAGAGCACTGGTAATATATGAGATGCATTCG 742  
Db |  
252 AAGCGACCTACCTCTTAAGTATATCCTCAAGAGCACTGGTAATATATGAGATGCATTCG 311  
QY 743 GTGGATTCAGACGATGATCAAGCAATGTAGACATCCGGTACTTTTCATTCGAGCTG 802  
Db |  
312 GTGGATTCAGACGATGATCAAGCAATGTAGACATCCGGTACTTTTCATTCGAGCTG 371  
QY 803 TGTCCAGCTTACTATTTCAGAGCTTGGAGTAAATTTGATTAATTAATGCCCTGCC 862  
Db |  
372 TGTCCAGCTTACTATTTCAGAGCTTGGAGTAAATTTGATTAATTAATGCCCTGCC 431  
QY 863 ATGAGTTCAAGAGCTGGAGTACTCAACCTCTTCCAAAGATGAATTTTGGGATATT 922  
Db |  
432 ATGAGTTCAAGAGCTGGAGTACTCAACCTCTTCCAAAGATGAATTTTGGGATATC 491  
QY 923 CTACCATAACTCTTTT 939  
Db |  
492 CTACCATAACTCTTTT 508

RESULT 10  
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LOCUS  
DEFINITION  
aestivum cDNA clone wholif13 3', mRNA sequence.

ACCESSION  
BJ272361  
VERSION  
BJ272361.1 GI:20037474  
KEYWORDS  
EST.

SOURCE  
Triticum aestivum (bread wheat)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae;  
Pooideae; Triticeae; Triticum.

1 (bases 1 to 564)

Ogihara, Y. and Murai, K.

Expressed genes in Triticum aestivum

Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1..564

FEATURES  
source

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## ORIGIN

Query Match 15.6%; Score 468.4; DB 12; Length 564;  
Best Local Similarity 95.5%; Pred. No. 4e-47; Mismatches 20; Indels 4; Gaps 3;  
Matches 512; Conservative 0;

QY 2429 AAAAGGGGGCAACAATACATACATG-CCATGATCTTATGTCAATTTTCCTCGGG 2487  
Db |  
564 AAAAGGGGGCAACAATACATACATGCTGCCATGATCTTATGTCAATTTTNGTGG 505  
QY 2488 ATAAAAAGAAACAATACCTGAGTTGACCGATTCCTGCTCATGACCAAAATCCGCA 2547  
Db |  
504 ATAAAAAGAAACAATACCTGAGTTGACCGATTCCTGCTCATGACCAAAATCCGCA 445  
QY 2548 AGGAGTGGGAGGCTCTGCGCTTGAGGACTTTCCAAAGCGCCAAAC-GGCTGAGTGGCAT 2606  
Db |  
444 AGGAGTGGGAGGCTCTGCGCTTGAGGACTTTCCAAAGCGCCAAACGGGCTGAGTGGCAT 385  
QY 2607 GGTCTATGACCTGGGAAGCCTGATTTGCTGAGAAATAGCCGATTCGTTGCCCTTTCCATG 2666  
Db |  
384 GGTCTATGACCTGGGAAGCCTGATTTGCTGAGAAATAGCCGATTCGTTGCCCTTTCCATG 325  
QY 2667 AAAGATGAAGACAGGCGGAGATCTATGTGGCTTCACACAGCCACTTACCGGCCCTT 2726  
Db |  
324 AAAGATGAAGACAGGCGGAGATCTATGTGGCTTCACACAGCCACTTACCGGCCCTT 265  
QY 2727 GTTGAGCTCCCAAGAGCGGCGCGGCTGGGAACCGGTGGGACACAGGCAAGCCA 2786  
Db |  
264 GTTGAGCTCCCAAGAGCGGCGGCTGGGAACCGGTGGGACACAGGCAAGCCA 205  
QY 2787 GCACATGAGCTTCCTCACCAGCAGCTTACTGATCGGCTCTCACCATACACAGTTC 2846  
Db |  
204 GCACATGAGCTTCCTCACCAGCAGCTTACTGATCGGCTCTCACCATACACAGTTC 145  
QY 2847 TCGCATTTCTCTACTTCCAACTTACCCCTGCTCAGCTACTGCTGCTATCTCTAGTA 2906  
Db |  
144 TCTCAITTTCTCACTTCCAACTTACCCCTGCTCAGCTACTGCTGCTATCTCTAGTA 85  
QY 2907 TTGCGCCCTGATTTTGAGAGCAATATATACAGTAAATAATATGCTATATGTA 2962  
Db |  
84 TTGCGCCCTGATTTTGAGAGC--GGATATACAGTAAATAATATGCTATATGTA 31

RESULT 11  
CAL199345

## LOCUS

## DEFINITION

## 5', mRNA sequence.

## ACCESSION

## CAL199345

## VERSION

## CAL199345.1

## KEYWORDS

## EST.

## SOURCE

## ORGANISM

## Saccharum officinarum

## Saccharum officinarum

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

## clade; Panicoideae; Andropogoneae; Saccharum.

## 1 (bases 1 to 697)

## Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P.

## The libraries that made SUCET

## Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

## COMMENT

## Contact: Arruda P



Centro de Biologia Molecular e Engenharia Genética  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information  
through the Brazilian Clone Collection Center (BCCC)  
<http://www.bccccenter.fcav.unesp.br>  
Plate: 01 row: G column: 11  
Seq primer: T7 Promoter Primer.

## FEATURES

source

## ORIGIN

Query Match	15.1%; Score 452.4; DB 14; Length 697;
Best Local Similarity	82.9%; Pred.No.3.1e-45;
Matches 529; Conservative 0; Mismatches 106; Indels 3; Gaps 1;	
QY	2304 GAAGAGAAATTCGCAAGATTGCTGTCAAAAGATTGAGGAAGACAGACAGATGCGCAATTTC 2363
DB	
QY	1 GAAGAGAAATTCGCAAGTTTGTGATCCGAAAGATTAAAGNAGAGGCAATGCGCAATTTT 60
DB	
QY	2364 TTTGTTTCTCATGTTTCTCAAGGAGTTCCAATGTTCTACATGGGTGATGAATATGCG 2423
DB	
QY	61 TTTGTTTCTGATGTTTCTCAGGAGTTCCAATGTTCTACATGGCGATGAATGGT 120
DB	
QY	2424 CACACAAAGGGGCAACACATACATCTGCGCATGATCTTTATGTCAATATTTTCGC 2483
DB	
QY	121 CACACAAAGGAGGAAACAAACAATACATCTGCGCATGACCATATGTCAATATTTTCGGT 180
DB	
QY	2484 TGGGATAAA--AAGAACAACTCTGAGTTGSCCGGATCTGCTGCCTCATGACCAA 2540
DB	
QY	181 TGGGATAAAGAGAGAACAACTCTTGATTTGTACAGATTCTGTCGGCTCATGACCAA 240
DB	
QY	2541 TTCGCAAGGAGTCGAGGGTCTTGCGCTTGAGGACTTTCCAAACGCCCAACGGCTGCAG 2600
DB	
QY	241 TTCGCAAGGAATGTGAATCTCTTGTTCTTGAGGACTTCCCGACTTCAGACGGTTGCA 300
DB	
QY	2601 TGGCATGTCTATGACTGCGGAGCCTGATGTGCTGAGAAATAGCGGATTTGTTGCCTTT 2660
DB	
QY	301 TGGCAGGTCTATCAGCTGCGGAGCCTGACTGTGTCGAGGCAAGCGGATTTGTTGCCTTC 360
DB	
QY	2661 TCCATGAAGATGAAGACAGGCGGAGATCTATGTGCGCTTCAACACAGGCACCTTACCG 2720
DB	
QY	361 ACCATGAAGGATGAACCAAGCGGAGATCTAGTGTGCGCTTCAACACAGGCACTGCGCC 420
DB	
QY	2721 GCGGTGTGTGAGCTCCACAGACGCGGAGCGCGCTGGGAACCGGTGGTGGACACAGGC 2780
DB	
QY	421 GTGGTTCGTGGGCTTCAGAGCGCCTTGTTTCOGATGGAGCCAGTGGTGGACACAGGC 480
DB	
QY	2781 AAGCAGCACCATAGGACTTCCTCACGAGGACTTACCTGATGCGGCTCTCACCATACAC 2840
DB	
QY	481 AAAGAAGCACCTATGACTTCTCTCACCGATGGTTTACACAGACCGTGTGTCAACGGTTTAC 540
DB	
QY	2841 CAGTCTTCGCAATTTCTTCTACTCCAACTCTACCCCATGCTCAGTACTCTCAACGGTCACTC 2900
DB	

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Db      541  CAGTCTCTTTCATTTCTCACTCCAAATCTCTACCCCTATGCTTAGCTACTCTCTTAATC 600
Qy      2901  CTAGTATTGCGCCCTCGATGTTTGAGAGACCAATATATA 2938
Db      601  CCTGTATTGCGCCCTCGATGTTTGAAAGAGAGAATATA 638

RESULT 12
CF041929
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF041929
QC131h03.yg QCI Zea mays 622 bp mRNA linear EST 17-JUL-2003
QC131h03.yg QCI Zea mays cDNA clone QC131h03, mRNA sequence.
CF041929
CF041929.1 GI:32937110
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 622)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Contact: Genoplante
Genoplante

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
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1..622
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ORIGIN

Query Match	14.4%	Score 431.2	DB 14	Length 622
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Db	8	TAAAGGAAGGCAAAATCGCA	AAATTTCTTTGTGTGCTTATGGTTTCTCAGGAGTTC	CAAA 67
QY	2398	TGTTTCTCATCGGTGATG	GAATATGGCCACACAAAGGGGGCAACAAACAATACATAC	TGCC 2457
Db	66	TGTTTCTCATGGGCGATGA	ATATGTCTCACAAAGGAGGAGAAACAATACGTA	CTGCC 127
QY	2458	ATGATTTCTTATGTCAA	TATTTTCGTCGGGATAAAA--AAGAACAAATACTCTG	AGTTGC 2514
Db	128	ATGACCATATGTCAACT	ATTTCCGTTGGGATAAGGAAGGAACAATCCCTCTG	ATTTGT 187
QY	2515	ACCGATTCTGTGCTCAT	GACCAAAATTCGCCAAGAGGTGCAGGAGTCTTGCCCTTG	AGG 2574
Db	188	ACAGATTCTGCGCTCT	CATGACCAAAATTCGCCAAGGAATGTGAATCTCTTGCGCCTTG	AGG 247
QY	2575	ACTTTCACGGCCAAACG	CTCGACTGCGTGCATCAGCCTGGGAGAGCCTGATTTGGT	2634
Db	248	ACTTCCCGACTTCAGA	ACGGTTGAAATGCGACGGTCTCAGCCCGGAAGCCTGACTGGT	307
QY	2635	CTGAGAAATAGCGGAT	TCGTTGCTTTTTCATGAAGATGAAAGACAGGCGGAGATCT	ATG 2694
Db	308	CAGAGGCAAGCCGAT	TCGTTGCTTTCCATATGAGGACGAACCAAGCGAGATCT	ACG 367
QY	2695	TGGGCTTCAACACACAG	CCACTTACCGGCGGTGTTGTGAGCTCCAGAGCGCGACGGCGCC	2754

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Db      368 TGGCTTCAACACAGTCACCTCCGGTGTGTGTCCGGCTTCCAGAGCGCTCTGGGTCC 427
Qy      2755 GGTGGGAACGGTGGTGGACACAGGCAAGCCAGCACCATACGACTTCCTCACCAGGACT 2814
Db      428 GATGGGAGCGGTGGTGGACACCGCAAGGAGGACCATATGACTTCCTCACCAGTGGCC 487
Qy      2815 TACCTGATCGGCTCTCACCATACACAGTTCTCGATTTCCCTACTCCTCAACCTTACC 2874
Db      488 TACAGATCGGTGTGCACGCTTACAGTTCTCTCATTTCTCAATCCAACTCTCTATC 547
Qy      2875 CCATGCTCAGTCTACTCATCGGTCTATCTAGTATTTGGCCCTGATGTTTGAGAGACCAATA 2934
Db      548 CTATGCTCAGTCTACTCTCTCCATCATCTTGTATTTGGCCCTGATGTTGAGAGAGCGGA 607
Qy      2935 TATA 2938
Db      608 TACA 611

RESULT 13
BU974414
LOCUS      BU974414
DEFINITION HB27N18r BC Hordeum vulgare subsp. vulgare cDNA clone HB27N18
5-PRIME, mRNA sequence.
ACCESSION  BU974414
VERSION     BU974414.1 GI:24225207
KEYWORDS   Hordeum vulgare subsp. vulgare
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
REFERENCE  1 (bases 1 to 445)
AUTHORS    Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.
TITLE      Barley ESTs from developing seeds
JOURNAL    Unpublished (2002)
COMMENT    Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel.: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 445 Std Error: 0.00
Plate: 27 row: N column: 18
Seq primer: M13rev.
Location/Qualifiers
1..445
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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/sub_species="vulgare"
/db_xref="GABI:239263"
/db_xref="taxon:112509"
/clone="HB27N18"
/tissue_type="developing caryopsis"
/dev_stage="8-15 DAP (days after pollination)"
/lab_host="XL10-Gold"
/clone_lib="BC"
/notes="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP (days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN
Query Match 13.8%; Score 414.2; DB 13; Length 445;
Best Local Similarity 97.0%; Pred. No. 1.5e-40;
Matches 422; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy      672 GTTTCATTGGGAAGCGGACCTACCTCTAAGATATCTCTCAAAAGGACCTGGTAATATGA 731
Db      11 GTTTCATTGGGAAGCGGACCTACCTCTAAGATATCTCTCAAAAGGACCTGGTAATATGA 70
Qy      732 GATGCACCTTGGTGGATTCAGAAAGCATGATTCAGCAATGTAGAAATCCGGGTACTTT 791
Db      71 GATGCACCTTGGTGGATTCAGAAAGCATGATTCAGCAATGTAGAAATCCGGGTACTTT 130
Qy      792 CATTGGAGCTGTGTCCGAAGCTTGACTATTTGAAGAGAGCTTGGAGTTAATTGTATTGAATT 851
Db      131 CATTGGAGCTGTGTCCGAAGCTTGACTATTTGAAGAGAGCTTGGAGTTAATTGTATTGAATT 190
Qy      852 AATGCCCTGCCATGATGTTCAACGAGCTGGAGTATGCAACCTCTCTTCCAAAGATGAACCT 911
Db      191 AATGCCCTGCCATGATGTTCAACGAGCTGGAGTATGCAACCTCTCTTCCAAAGATGAACCT 250
Qy      912 TTGGGGATATTTCTACCATATAAACTCTTTTCCACATGACAAAGATACACATCAGCGGGAT 971
Db      251 TTGGGGATATTTCTACCATATAAACTCTTTTCCACATGACAAAGATACACATCAGCGGGAT 310
Qy      972 AAAAAAATGTTGGCGGTGATGCCATAAATGAGTTTCAAAACTTTTGTAGAGAGGCTCACAA 1031
Db      311 AAAAAAATGTTGGCGGTGATGCCATAAATGAGTTTCAAAACTTTTGTAGAGAGGCTCACAA 370
Qy      1032 ACGGGGAATTGAGGTGATCCTGGATGTTGTTTCAACCATACAGCTGAGGGTAATGAGAA 1091
Db      371 ACGGGGAATTGAGGTGATCCTGGATGTTGTTTCAACCATACAGCTGAGGGTAATGAGAA 430
Qy      1092 TGGTCCAATATTATC 1106
Db      431 TGGTCCGATATTATC 445

RESULT 14
BU971179
LOCUS      BU971179
DEFINITION HB16N12r BC Hordeum vulgare subsp. vulgare cDNA clone HB16N12
5-PRIME, mRNA sequence.
ACCESSION  BU971179
VERSION     BU971179.1 GI:24221972
KEYWORDS   Hordeum vulgare subsp. vulgare
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
REFERENCE  1 (bases 1 to 438)
AUTHORS    Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.
TITLE      Barley ESTs from developing seeds
JOURNAL    Unpublished (2002)
COMMENT    Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel.: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 438 Std Error: 0.00
Plate: 16 row: N column: 12
Seq primer: M13rev.
Location/Qualifiers
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/sub_species="vulgare"
/db_xref="GABI:236011"
/db_xref="taxon:112509"
/clone="HB16N12"
/tissue_type="developing caryopsis"
/dev_stage="8-15 DAP (days after pollination)"
/lab_host="XL10-Gold"

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/clone_lib="BC"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); developing
carypsopsis, 8-15 DAP (days after pollination) Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable."

```

## ORIGIN

```

Query Match      13.6%; Score 408.4; DB 13; Length 438;
Best Local Similarity 96.1%; Pred. No. 7.3e-40;
Matches 416; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 941 CACCAATGACAGATACACATCAGGCGGGGATAAAAACTGTGGCGTGATGCCATAAATG 1000
Db 4 CACGAGGACGAGATACACATCAGGCGGGGATAAAAACTGTGGCGTGATGCCATAAATG 63

Qy 1001 AGTTCAAAACCTTTTGAAGAGAGGCTCACAACGGGGAAATTGAGGTGATCCTGGATGTTG 1060
Db 64 AGTTCAAAACCTTTTGAAGAGAGGCTCACAACGGGGAAATTGAGGTGATCCTGGATGTTG 123

Qy 1061 TCTTCAACCATACAGCTGAGGCTGAATGAGAAATGCTCCAAATATTATCATTTAAGGGGGTGC 1120
Db 124 TCTTCAACCATACAGCTGAGGCTGAATGAGAAATGCTCCAAATATTATCATTTAAGGGGGTGC 183

Qy 1121 ATAATACATACATATATGCTTGCACCCAGGAGGATTTTATACATTTCTGGCTGTG 1180
Db 184 ATAATACATACATATATGCTTGCACCCAGGAGGATTTTATACATTTCTGGCTGTG 243

Qy 1181 GGAATACCTTCAAGTGAATCATCTGCTGCTGCTCAATTCATTTAGATTTGTTAAGAT 1240
Db 244 GGAATACCTTCAAGTGAATCATCTGCTGCTGCTCAATTCATTTAGATTTGTTAAGAT 303

Qy 1241 ACTGGGTGACGGAATGATGTTGATGTTTTCGTTTGTGATCTTGATCCATAATGACCA 1300
Db 304 ACTGGGTGATGGAATGATGTTGATGTTTTCGTTTGTGATCTTGATCCATAATGACCA 363

Qy 1301 GAGGTTCCAGTCTGTGGATCCAGTTAACTGTATGGAGCTCCAAATAGAGGTGACATCA 1360
Db 364 GAGGTTCCAGTCTGTGGATCCAAATTAACGTGTATGGAGCTCCAAATAGAGGTGACATCA 423

Qy 1361 TCACACAGGGACAC 1375
Db 424 TCACACAGGGACAC 438

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RESULT 15
BU971450
LOCUS BU971450.1 BC Hordeum vulgare subsp. vulgare cDNA clone HB17K14
DEFINITION BU971450.1 BC Hordeum vulgare subsp. vulgare cDNA clone HB17K14
5-PRIME, mRNA sequence.
ACCESSION BU971450
VERSION BU971450.1 GI:24222243
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Hordeum.
1 (bases 1 to 438)
Rachuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de

```

```

Insert Length: 438 Std Error: 0.00
Plate: 17 row: K column: 14
Seq primer: M13rev.
Location/Qualifiers
source
1..438
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:236284"
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/clone="HB17K14"
/tissue_type="developing carypsopsis"
/dev_stages="8-15 DAP (days after pollination)"
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/clone_lib="BC"

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## FEATURES

## source

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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); developing
carypsopsis, 8-15 DAP (days after pollination) Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present, as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable."

```

## ORIGIN

```

Query Match      13.6%; Score 407.6; DB 13; Length 438;
Best Local Similarity 96.7%; Pred. No. 9.1e-40;
Matches 416; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 802 GTGTGCGAGCTTGACTATTTGAAGAGCTTTGGAGTTAATTGATTAATTAATGCCCTGC 861
Db 9 GGTTCGAGCTTGACTATTTGAAGAGCTTTGGAGTTAATTGATTAATTAATGCCCTGC 68

Qy 862 CATGAGTTCAACGAGCTGGAGTACTCAACCTCTTCTTCAAGATGACCTTTTGGGATAT 921
Db 69 CATGAGTTCAACGAGCTGGAGTATGCAACCTCTTCTTCAAGATGACCTTTTGGGATAT 128

Qy 922 TCTACCATAACTCTTTTCCACCAATGACAAAGATACACATCAGCGGGGATAAAAACTGT 981
Db 129 TCTACCATAACTCTTTTCCACCAATGACCGAGATACACATCAGCGGGGATAAAAACTGT 188

Qy 982 GGGCGTGATGCCATAAATAGAGTTCAAAACTTTTGTAAAGAGAGGCTCAAAACCGGGAAAT 1041
Db 189 GGGCGTGATGCCATAAAGAGTTCAAAACTTTTGTAAAGAGAGTCTCAAAACCGGGAAAT 248

Qy 1042 GAGGTGATCCTGGATGTTGTCTTCAACCATACAGCTGAGGTTAATGAGATGGTCCAATA 1101
Db 249 GAGGTGATCCTGGATGTTGTCTTCAACCATACAGCTGAGGTTAATGAGATGGTCCAATA 308

Qy 1102 TTATCATTTAAGGGGGTGCATAATACATACATATATGTTTGCACCCAGGAGAGTTT 1161
Db 309 TTATCATTTAAGGGGGTGTGATAATACATACATATATGTTTGCACCCAGGAGAGTTT 368

Qy 1162 TATAACTATTCTGCTGTGGGAATACCTTCAACTGTAAATCATCTGTGGTTGTCATTC 1221
Db 369 TATAACTATTCTGCTGTGGGAATACCTTCAACTGTAAATCATCTGTGGTTGTCATTC 428

Qy 1222 ATTGTAGATT 1231
Db 429 ATTGTAGATT 438

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Search completed: August 9, 2004, 22:04:07
Job time : 7312 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 9, 2004, 22:08:10 ; Search time 7673 Seconds

(without alignments)  
4315.662 Million cell updates/sec

Title: US-09-674-817B-3

Perfect score: 4212

Sequence: 1 SGPAFLRRWRPNATAGKV.....SNLYPMLSYSSVILVLRPDV 764

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n\_model -DEV=xlh

-Q=/cgn2\_1/USPTO.spool/US09674817/runat\_04082004\_165844\_24581/app\_query.fasta\_1.903

-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIPST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US09674817@cgn 1 1 4892 @runat\_04082004\_165844\_24581 -NCPU=6 -ICPU=3

-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_btg.\*

3: gb\_in.\*

4: gb\_cm.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rnd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4203	99.8	2590	8	AF438328	AF438328 Triticum
2	4154	98.6	2490	8	TAE301647	TAE301647 Triticum
3	4148	98.5	2437	6	AX010486	AX010486 Sequence
4	4120.5	97.8	2574	8	AF548380	AF548380 Triticum
5	4050	96.2	2997	6	AX010481	AX010481 Sequence
6	4050	96.2	2997	6	AX010482	AX010482 Sequence
7	4050	96.2	2997	8	TAE307689	TAE307689 Triticum
8	4015.5	95.3	2495	8	AF490375	AF490375 Hordeum v
9	4005.5	95.1	2584	8	AB074189	AB074189 Hordeum v
10	3988.5	94.7	2445	8	AF490376	AF490376 Hordeum v
11	3586	85.1	2288	8	AB015615	AB015615 Oryza sat
12	3569.5	84.7	2700	6	AR427894	AR427894 Sequence
13	3528.5	83.8	2712	6	AR072143	AR072143 Sequence
14	3528.5	83.8	2712	6	ZMU18908	U18908 Zea mays Su
15	3029	71.9	2706	6	AR241384	AR241384 Sequence
16	3029	71.9	2706	6	AX006091	AX006091 Sequence
17	3029	71.9	2706	6	BD080223	BD080223 Starch de
18	3029	71.9	2706	8	AV132996	AV132996 Solanum t
19	3001	71.2	1708	8	AF143589	AF143589 Hordeum v
20	2923	69.4	2806	6	AR241388	AR241388 Sequence
21	2923	69.4	2806	6	AX006100	AX006100 Sequence
22	2923	69.4	2806	6	BD080227	BD080227 Starch de
23	2918	69.3	1706	6	AX031277	AX031277 Sequence
24	2895.5	68.7	2352	6	AX505523	AX505523 Sequence
25	2895.5	68.7	2352	6	AX651353	AX651353 Sequence
26	2895.5	68.7	2352	8	BT010348	BT010348 Arabidops
27	2895.5	68.7	2694	8	BT000443	BT000443 Arabidops
28	2800	66.5	9643	8	AF548379	AF548379 Aegilops
29	2612	62.0	2133	6	A93395	A93395 Sequence 1
30	2612	62.0	2133	6	AR161657	AR161657 Sequence
31	2507.5	59.5	10352	8	AP005509	AP005509 Oryza sat
32	2493.5	59.2	10209	8	AB093426	AB093426 Oryza sat
33	2359.5	56.0	9289	6	AX031278	AX031278 Sequence
34	2359	53.6	1501	8	AF490377	AF490377 Hordeum v
35	2256	53.6	1517	8	AF438329	AF438329 Triticum
36	2234	53.0	11779	8	AF030882	AF030882 Zea mays
37	2228	52.9	10753	8	AV146807	AV146807 Zea mays
38	2228	52.9	10817	8	AV146808	AV146808 Zea mays
39	2218	52.7	10733	8	AV146812	AV146812 Zea mays
40	2218	52.7	10835	8	AV146811	AV146811 Zea mays
41	2206	52.4	10851	8	AV146810	AV146810 Zea mays
42	2165.5	51.4	10855	8	AV146800	AV146800 Zea mays
43	2152.5	51.1	10839	8	AV146796	AV146796 Zea mays
44	2152.5	51.1	10856	8	AV146791	AV146791 Zea mays
45	2152.5	51.1	10856	8	AV146797	AV146797 Zea mays

ALIGNMENTS

RESULT 1

AF438328 2590 bp mRNA linear PLN 13-NOV-2001  
LOCUS Triticum aestivum isomylase precursor, mRNA, complete cds;  
DEFINITION alternatively spliced.  
ACCESSION AF438328  
VERSION AF438328.1 GI:16905062  
KEYWORDS Triticum aestivum (bread wheat)  
SOURCE Triticum aestivum  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 2590)  
AUTHORS Netrphan,S., Khandelwal,R.L. and Chibbar,R.N.  
TITLE Characterization of isomylase transcripts produced during wheat  
JOURNAL grain development and germination  
REFERENCE 2 (bases 1 to 2590)  
AUTHORS Netrphan,S., Khandelwal,R.L. and Chibbar,R.N.  
TITLE Direct Submission  
JOURNAL Submitted (22-OCT-2001) Plant Biotechnology Institute, 110  
AUTHORS Gymnasium Place, Saskatoon, SK S7N 0W9, Canada  
FEATURES  
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MCHFEINLEYSTSSKMGFWGYSTINFFSPMRTYSGICKNCGDAINEFTFVREA  
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Pred. No.: 0 Length: 2590  
Score: 4203.00 Matches: 762  
Percent Similarity: 99.87% Conservative: 1  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.79% Indels: 0  
DBs: 8 Gaps: 0  
US-09-674-817B-3 (1-764) x AF438328 (1-2590)  
1 SerGlyProAlaProArgLeuArgTTPArgProAsnAlaThrAlaGlyVal 20  
Ddb |||||  
2 CGGGGCGGGCGCGCGCTCGACGGTGGCACCAATGCCACGCGGGGAGGGGTC 151  
Y |||||  
21 GlyGluValCysAlaAlaValValGluAlaAlaThrLysValLcluspGluGlyGluGlu 40

Qy	401	GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle	420
Db	1292	GGTTCAGTCTGTGGGATCCAGTTAAAGTGTATGGAGCTCCAATAGAAGTGCATGATC	1351
Qy	421	ThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIle	440
Db	1352	ACAAAGGAGACCTCTTGTTTACTCCACCACTTATTGACATGATCACAATGACCCCAATT	1411
Qy	441	LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGly	460
Db	1412	CTTGGAGCGCTCAAGCTCATTTGCTGGAAGCATGGGATCGAGAGGCGCTCTATCAAGTAGGT	1471
Qy	461	GlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArg	480
Db	1472	CAATTCCCTCCTCGAATGTTTGCTCTGAGTGGNATGGGAAGTACCCGGACATTTGCCGT	1531
Qy	481	GlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySer	500
Db	1532	CAATTCAATAAAGGCATGTATGGATTTCGCTGGTTCGTTCCGAATCTCTTTGTGGAAGT	1591
Qy	501	ProHisLeuTyrGlnAlaGlyGlyArgGlyProTrpHisSerIleAsnPheValCysAla	520
Db	1592	CCACACTTATCCAGCAGGAGGAGGAACCTTGGCACAGTATCAACTTTGTATGTGCA	1651
Qy	521	HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn	540
Db	1652	CATGATGCAATTTACACTGGCTGATTTGGTAAACATATAATAAGAAGTACAATTTACCAAAAT	1711
Qy	541	GlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGly	560
Db	1712	GGGAGAGAACACAGAGATGGAGAAATCACAACTTTAGCTGGAAATTTGGGGAGGAAGGA	1771
Qy	561	GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheVal	580
Db	1772	GAAATTCGAAGATTGTCTGTCAAAAGATTGAGGAAGAGGCAGATGCGCAATTTCTTTGTT	1831
Qy	581	CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr	600
Db	1832	TGCTCTATGGTTTCTCAAGGAGTTCCAAATGTTCTACATGGGTGAATATGGCCACACA	1891
Qy	601	LysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAsp	620
Db	1892	AAAGGGGGCAACAACATATATACGCGATGATTTCTATGTCATTTATTTTCGCTGGGAT	1951
Qy	621	LysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLys	640
Db	1952	AAAAAAGAACAATACTCTGAGTTCGACCGAATCTGCTGCCTCATGACCAATTCGCAAG	2011
Qy	641	GluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGly	660
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Qy	661	HisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLys	680
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Qy	681	AspGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValVal	700
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Qy	701	GluLeuProGluArgAlaGlyArgArgTrpGluProValValAspThrGlyLysProAla	720
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Qy	721	ProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSer	740
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Qy	741	HisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeu	760
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2372 CGCCCTGATCT 2383

RESULT 2

TAE301647 2490 bp mRNA linear PLN 04-JUN-2003

LOCUS Triticum aestivum mRNA for isoamylase (isol gene).

DEFINITION Triticum aestivum mRNA for isoamylase (isol gene).

ACCESSION AJ301647

VERSION AJ301647.1 GI:17932897

KEYWORDS isol gene; isoamylase.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1

REFERENCE Genschel,U., Gernot,A., Lorz,H. and Luetticke,S.  
AUTHORS The sugary-type isoamylase in wheat: tissue distribution and  
TITLE subcellular localisation  
JOURNAL Oncogene Publication  
REMARK Plants, DOI 10.1007/s00435-001-0691-3  
2 (bases 1 to 2490)

Direct Submission  
AUTHORS Genschel,U.  
TITLE Submitted (22-NOV-2000) Genschel U., Institut fuer Allgemeine  
JOURNAL Botanik, AMP II, Universitaet Hamburg, Ohnhorststrasse 18, Hamburg,  
26009 Germany  
REMARK revised by submitter 22-MAR-2001  
COMMENT Related entry AJ307685.

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10





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Qy	722	TyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHis	741
Db	2232	TAGCACTTCCTCACTGACGACTTACCTGATCGCGCTCTCACCATACACCAAGTTCTCTCAT	2291
Qy	742	PheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArg	761
Db	2292	TTCTCAACTCCAACTCTACCCCATGCTCAGCTACTCATCGGTCACTCCTAGTAGTGGCG	2351
Qy	762	ProAspVal	764
Db	2352	CCTGATGTT	2360

RESULT 3					
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LOCUS	AX010486	2437 bp	DNA	linear	PAT 06-SEP-2000
DEFINITION	Sequence 6 from Patent WO9958690.				
ACCESSION	AX010486				
VERSION	AX010486.1	GI:9997329			

GENUS	<i>Triticum aestivum</i> (bread wheat)
SOURCE	<i>Triticum aestivum</i>
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
REFERENCE	1
AUTHORS	Lueticke, S., Abel, G., Loerz, H. and Genschel, U.
TITLE	Nucleic acid molecules which code for enzymes derived from wheat and which are involved in the synthesis of starch
JOURNAL	Patent: WO 9958690-A 6 18-NOV-1999; LUETTICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE); GENSCHEL ULRICH (DE); HOECHST SCHERING AGREVO GMBH (DE)

## ORIGIN

Alignment Scores:

Alignment Scores:					
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Score:	4148.00	Matches:	750		
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Best Local Similarity:	98.43%	Mismatches:	7		
Query Match:	98.48%	Indels:	0		
DB:	6	Gaps:	0		

US-09-674-817B-3 (1-764) x AX010486 (1-2437)

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Qy		23	ValCysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluAspGlu	42
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Qy		43	ProValAlaGluAspArgTyrAlaLeuGlyValCysArgValLeuAlaGlyMetPro	62
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Qy		63	AlaProLeuGlyAlaThrAlaLeuAlaGlyValAsnPheAlaValTyrSerGlyCyl	82
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Qy		103	GluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIle	122
Dd		316	GAGGAGTTCCCTTGACCCCTCATGAATCGGACTGGGAACGATAGGCATGTCTTCATC	375
Qy		123	GluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheaspGlyThrPheAlaProHis	142
Dd		376	GAAGCGAGCTGCAGGACATGCTTTACGGGTACAGGTTTCAGCGCACCTTTGCTCTCTCAC	435
Qy		143	CysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaValile	162
Dd		436	TGCGGCACCTACCCTTGATGTTCCTCAATGTGTGTGTGGATCCTTATGTAAGCGAGTGATA	495
Qy		163	SerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCystTrpProGlnMetAlaGly	182
Dd		496	ACCGGAGGAGATAGTGTTTCGGCGCGTGTAAACAATTGCTGGCCTCAGATGGCTGGC	555
Qy		183	MetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrPro	202
Dd		556	ATGATCCCTCTTCCATATAGCACGTTTTGATTTGGGAAGCGACCTTACCTCTAAGATATCCT	615
Qy		203	GlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSer	222
Dd		616	CAAAGGACCTGGTAAATATAGATGCACCTTGGCTGGATTTCAGAACGATGATTCAAAC	675
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Dd		676	AATGTAGAACATCCCGGTACTTTTCATTTGGGCTGTCTCGAAGCTTGACTATTTCAAGGAG	735
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 LOCUS AF548380 2574 bp mRNA linear PLN 29-MAY-2003  
 DEFINITION Triticum aestivum isoamylase wDBE-D1 mRNA, complete cds.  
 ACCESSION AF548380  
 VERSION AF548380.1 GI:31096627  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 Poideae; Triticeae; Triticum.  
 REFERENCE 1 (bases 1 to 2574)  
 AUTHORS Rahman,S., Nakamura,Y., Li,Z., Clarke,B., Fujita,N., Mukai,Y.,  
 Yamamoto,M., Regina,A., Tan,Z., Kawasaki,S. and Morell,M.  
 TITLE The sugary-type isoamylase gene from rice and Aegilops tauschii:  
 characterization and comparison with maize and Arabidopsis  
 JOURNAL Genome 46 (3), 496-506 (2003)  
 REFERENCE 2 (bases 1 to 2574)  
 AUTHORS Rahman,S., Li,Z., Clarke,B., Regina,A. and Morell,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-Sep-2002) Plant Industry, CSIRO, Clunies Ross,  
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## ORIGIN

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US-09-674-817B-3 (1-764) x AF548380 (1-2574)



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RESULT 5
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DEFINITION Sequence 1 from Patent WO9958690.
ACCESSION AX010481
VERSION AX010481.1 GI:9997324
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE 1
AUTHORS Luetticke, S., Abel, G., Loerz, H. and Genschel, U.
TITLE Nucleic acid molecules which code for enzymes derived from wheat
JOURNAL Patent: WO 9958690-A 1 18-NOV-1999;
LUETTICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);
GENSCHEL ULRICH (DE); HOSCHT SCHERING AGREVO GMBH (DE)
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US-09-674-817B-3 (1-764) x AX010481 (1-2997)

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## RESULT 6

AX010482

LOCUS

AX010482

DEFINITION

Sequence 2 from Patent WO9558690.

ACCESSION

AX010482

VERSION

AX010482.1

KEYWORDS

GI:9997326

SOURCE

Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum

REFERENCE

1.

AUTHORS

Lueticke,S., Abel,G., Loerz,H. and Genschel,U.

TITLE

Nucleic acid molecules which code for enzymes derived from wheat

JOURNAL

and which are involved in the synthesis of starch

Patent: WO 9558690-A 2 18-NOV-1999;

LUETTICKE STEPHANIE (DE); ABEL GERNOT (DE); LOERZ HORST (DE);

GENSCHEL ULRICH (DE); HOECHST SCHERING AGREVO GMBH (DE)

FEATURES

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ORIGIN

source

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ACCESSION	AJ307689		
VERSION	AJ307689.1 GI:14331017		
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AUTHORS	Genschel,U., Gernot,A., Lorz,H. and Luetticke,S.		

TITLE	The sugary-type isoamylase in wheat: tissue distribution and subcellular localisation			
JOURNAL	Online Publication			
REMARK	Planta, DOI 10.1007/s00425-001-0591-3			
REFERENCE	2			
AUTHORS	Genschel,U., Abel,G., Lorz,H. and Luetticke,S.			
TITLE	The sugary-type isoamylase in wheat			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 2997)			
AUTHORS	Luetticke,S.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-JUN-2001) Luetticke S., Insitut fuer Allgemeins Botanik, Universitaet Hamburg, Ohnhorststrasse 18, Hamburg, 20609, GERMANY			
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Qy      751 uSerTyrSerSerValIleLeuValLeuArgProAspVal 764
Db      2882 CAGCTACTCATCGTCTATCTAGTATTGGCCCTGATGTT 2921

RESULT 8
AF490375
LOCUS      Hordeum vulgare subsp. vulgare mRNA linear PLN 25-JUL-2002
DEFINITION Hordeum vulgare isoamylase mRNA, complete cds.
ACCESSION AF490375
VERSION    AF490375.1 GI:21314274
KEYWORDS   .
SOURCE     Hordeum vulgare subsp. vulgare
ORGANISM   Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 2495)
            Burton,R.A., Jenner,H., Carrangis,L., Fahy,B., Fincher,G.B.,
            Hylton,C., Laurie,D.A., Parker,M., Waite,D., van Wegen,S.,
            Verhoeven,T. and Denyer,K.
            Starch granule initiation and growth are altered in barley mutants
            that lack isoamylase activity
            Plant J. 31 (1), 97-112 (2002)

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MEDLINE  22096154
PUBMED   12100486
REFERENCE 2 (bases 1 to 2495)
AUTHORS  Burton,R.A., Denyer,K. and Fincher,G.B.
TITLE    Direct Submission
JOURNAL  Submitted (06-MAR-2002) Plant Science, University of Adelaide,
        Waite Campus, Urrbrae, SA 5064, Australia
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Pred. No.:      0      Length:      2495
Score:          4015.50      Matches:      724
Percent Similarity: 97.25%      Conservative: 19
Best Local Similarity: 94.76%      Mismatches: 20
Query Match:      95.33%      Indels:      1
DB:              8      Gaps:      1
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Qy      22 GluValCysAlaAlaValValGluAlaAlaThrLysVal---GluAspGluGlyGluGlu 40
Db      202 GAGGTCTGCGCGCGCGCTCGAGCGCGCAGCGCGCGAGAGGAGGAGGAGGAG 261
Qy      41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgValLeuAlaGly 60
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Qy      81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArg 100
Db      382 GCGGAGGACCGCGCGCTGCGCTCTTTCACGCCAGAGATCTCAAGCGCGGATAGG 441
Qy      101 ValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTyrHisVal 120
Db      442 GTGAGCGAGGAGGTTCCTCCCTTGACCCCTGATCGACTGGGAGCGTGGCATGTC 501
Qy      121 PheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAla 140

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 161 ValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMet 180  
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 682 GCTGGCATGATCCCTCTCCATATAGCACCTTTGATTTGGGAAGCGACCTACCTCTAAGA 741  
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 221 SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeu 240  
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 922 TATGCAACCTCTCTCCAGATGAACCTTTTGGGGATATTCACCAATAAATCTTTTCA 981  
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## RESULT 9

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 LOCUS Hordeum vulgare hvisol gene for isoamylase, complete cds.  
 DEFINITION  
 AB074189  
 ACCESSION  
 AB074189.1 GI:16923278  
 KEYWORDS  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 REFERENCE  
 1 Komatsu, A., Kato, T. and Komae, K.  
 AUTHORS Isolation of isoamylase gene in barley  
 TITLE Published Only in Database (2001)  
 JOURNAL

REFERENCE	2 (bases 1 to 2584)	Db	418	GGCGAGGACCGCGCGTCTGCTCTTACGCCAGAGATCTCAAGCGCGATAGG	477
AUTHORS	Komatsu,A. and Komae,K.	Qy	101	ValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisVal	120
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JOURNAL	Submitted (12-NOV-2001) Akira Komatsu, National Institute of Crop Science, Laboratory of Wheat and Barley Quality: 2-1-18 Kannondai, Tsukuba, Ibaraki 305-8518, Japan (E-mail:akomatsu@naro.affrc.go.jp, URL:http://nics.naro.affrc.go.jp/, Tel:81-298-38-8949, Fax:81-298-38-8949)	Qy	121	PhelLeGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAla	140
FEATURES	Location/Qualifiers	Db	538	TTCTTCGAAGCGAGCTGACGGCATGCTTATGGGTACAGTTTCGACGGCACCTTCGCT	597
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transit_peptide	103..246	Db	898	AAGAGCTTGAGGTTAATGTATAGATAATTAATGCCCTGCCCATGAGTTCAACGAGCTGGAG	957
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	/product="unnamed"	Db	1018	CCAATGACGAGATACAGTCAGGTGGGATATAAAACCTGTGGCGGTGATGGCATAAACGAG	1077
ORIGIN		Qy	301	PhelysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal	320
Alignment Scores:		Db	1078	TTCAAACTTTTGAAGAGAGTCTCACAAACGGGGATTTAGGTAATCTTGATGTTGTC	1137
Pred. No.:	0	Qy	321	PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp	340
Score:	4005.50	Db	1138	TTCAACCATACAGCTGAGGTAATGAGAAATGGTCCGATATTATCATTTAGGGGGTTGAT	1197
Percent Similarity:	97.12%	Qy	341	AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly	360
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Query Match:	95.10%	Qy	361	AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr	380
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Db	178 GGCGCGCGCGCGCTGCGACGATGCGGCCCAATGCGACGCGCGGAGGGGTTCGGC	Qy	401	GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle	420
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Db	238 GAGGTCTGCGCGCGCGCTGAGGCGCGACGAGCGCGGAGGAGGAGGAGGAGGAG	Qy	421	ThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIle	440
Qy	41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyValaCysArgValLeuAlaGly	Db	1438	ACAACAGGAGCACCTCTTGTACTCCACCACTATTGACATGATCAGCAATGACCCCAATT	1497
Db	298 GAGAGCGCGTCTGAGGACAGTATGCGTTCGAGAGCGCGCTGACAGGTGCTCCCGGA	Qy	441	LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGly	460
Qy	61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer	Db			
Db	358 ATGCCCGCGCGCTGCGCGCACCGCGCTCGCGCGCGGGTCAATTTGCGCGCTACTCA	Qy			
Qy	81 GlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArg				

Db 1498 CTTGGAGCGCTCAAGCTCATTTGCTGAAGCATGGATGCGAGGCGCTCTCTCAAGTAGT 1557  
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 Db 2038 AAAAAAGAAACACTCTGACTTGACCCGATTCCTGCTGCTCATGCCAAATTTCCGCAAG 2097  
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## RESULT 10

LOCUS AF490376 2445 bp RNA linear PLN 25-JUL-2002  
 DEFINITION Hordeum vulgare mutant isomylase precursor RNA, complete cds.  
 ACCESSION AF490376  
 VERSION AF490376.1 GI:21314276  
 KEYWORDS

SOURCE Hordeum vulgare  
 ORGANISM Hordeum vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Triticeae; Hordeum.  
 REFERENCE 1 (bases 1 to 2445)  
 AUTHORS Burton,R.A., Jenner,H., Carrangis,L., Fahy,B., Fincher,G.B.,  
 Hyton,C., Laurie,D.A., Parker,M., Waite,B., van Wegen,S.,  
 Verhoeven,T. and Denyer,K.  
 TITLE Starch granule initiation and growth are altered in barley mutants  
 that lack isomylase activity  
 JOURNAL Plant J. 31 (1), 97-112 (2002)  
 MEDLINE 22096154  
 PubMed 12100486  
 REFERENCE 2 (bases 1 to 2445)  
 AUTHORS Burton,R.A., Denyer,K. and Fincher,G.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-MAR-2002) Plant Science, University of Adelaide,  
 Waite Campus, Urrbrae, SA 5064, Australia  
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## ORIGIN

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QY	121	PheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAla	140
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DB	679	TATCCTCAAAAGGACCTTGTAATATATGAGATGCACCTTCGTGGATTCACGAAGCATGAT	738
QY	221	SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeu	240
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 VERSION AB015615.1 GI:3252793  
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 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1  
 AUTHORS Fujita, N., Kubo, A., Francisco, P. B. Jr., Nakakita, M., Harada, K.,  
 Minaka, N., and Nakamura, Y.  
 TITLE Purification, characterization, and cDNA structure of isoamylase  
 from developing endosperm of rice  
 JOURNAL Planta 208 (2), 283-293 (1999)  
 MEDLINE 99266133  
 PUBMED 1033591  
 REFERENCE 2 (bases 1 to 2288)  
 AUTHORS Nakamura, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-JUN-1998) Yasunori Nakamura, National Institute of  
 Agrobiological Resources, Department of Plant Physiology, 2-1-2  
 Kannondai, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail:nakayn@affrc.go.jp, Tel:81-298-38-8382,  
 Fax:81-298-38-8347)  
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ACCESSION AR427894  
VERSION AR427894.1 GI:40186914  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
TITLES 1 (bases 1 to 2700)  
AUTHORS Swalt,V.J.H. and Singletary,G.W.  
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 1 (bases 1 to 2712)  
 James M.G., Robertson, D.S. and Myers, A.M.  
 Characterization of the maize gene sugary1, a determinant of starch composition in kernels  
 Plant Cell 7 (4), 417-429 (1995)  
 JOURNAL 95290995  
 MEDLINE 773016  
 PUBMED  
 REFERENCE 2 (bases 1 to 2712)  
 MYERS, A.M.  
 Direct Submission  
 Submitted (19-DEC-1994) Alan M. Myers, Biochemistry and Biophysics, Iowa State University, 2110 Molecular Biology Building, Ames, IA 50011, USA  
 JOURNAL  
 COMMENT On Apr 6, 1995 this sequence version replaced gi:755295.  
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## ORIGIN

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ACCESSION AR241384  
VERSION AR241384.1 GI:27287051  
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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2706)  
AUTHORS Edwards, E.A., Smith, A.M., Martin, C.R. and Bustos Guillen, R.  
TITLE Starch debranching enzymes  
JOURNAL Patent: US 6469230-A 2 22-OCT-2002;  
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 9, 2004, 22:04:15 ; Search time 728 Seconds

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Maximum Match 100%  
Listing first 45 summaries

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10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	3515.5	83.5	2715	6	Aad42890 Maize sug
5	3029	71.9	2706	2	Aax27061 S. tubero
6	2923	69.4	2806	2	Aax27066 Original
7	2918	69.3	1706	2	Aax34654 Partial c
8	2855.5	68.7	2352	6	Abz12413 Arabidops

9	2895.5	68.7	2352	7	ADA67900	Ada67900 Arabidops
10	2612	62.0	2133	2	AAT96754	Aat96754 S. tubero
11	2359.5	56.0	9289	2	AAX34655	Aax34655 Hexaploid
12	2234	53.0	11779	6	RAA42891	Aad42891 Maize sug
13	2179	51.7	10439	6	RAA47817	Aad47817 Alternati
14	1884	44.7	1663	2	AAX33162	Aax33162 Potato is
15	1577	37.4	2634	2	AAX27062	Aax27062 S. tubero
16	1487	35.3	2370	7	ADA71085	Ada71085 Rice gene
17	1379	33.2	4745	6	ABS54601	AbS54601 Synchoco
18	1305.5	31.0	1995	6	ABL92608	AbI92608 Chlamydia
19	1305.5	31.0	1995	7	ACA30742	ACA30742 Prokaryot
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21	1305.5	31.0	273254	3	AAc81914	AAc81914 Chlamydia
22	1300	30.9	1998	6	ABL92637	AbI92637 Chlamydia
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24	1264	30.0	2001	7	ACA31084	ACA31084 Prokaryot
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29	1204	28.6	349980	5	AAH68531	Aah68531 C Glutami
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32	1149.5	27.3	2151	7	ABT14630	Abt14630 Pseudomon
33	1062.5	25.2	22934	4	AA559613	Aa559613 Propionib
34	1062.5	25.2	22934	7	ACF64542	ACf64542 Propionib
35	1032.5	24.5	1389	2	AAZ27067	Aax27067 Original
36	1014	24.1	1980	7	ACA34446	ACA34446 Prokaryot
37	1014	24.1	110000	2	AAT42063_14	Continuation (15 o
38	996	23.6	1989	7	ACA42966	ACA42966 Prokaryot
39	980.5	23.3	1965	4	AA556077	Aa556077 Salmonell
40	971	23.1	1913	4	AAf71541	Aaf71541 Corynebac
41	915.5	21.7	2843	2	AAZ27060	Aax27060 S. tubero
42	910.5	21.6	2843	2	AAZ27065	Aax27065 Original
43	890	21.1	2649	6	ABZ12474	Abz12474 Arabidops
44	830.5	19.7	603	9	ADC08661	Adc08661 Wheat DNA
45	825	19.6	2325	2	AAT95400	Aat95400 Flavobact

ALIGNMENTS

RESULT 1

AAZ24492

ID AAZ24492 standard; DNA; 2997 BP.

XX

AC AAZ24492;

XX

DT 18-FEB-2000 (first entry)

XX

DE Wheat isoamylase cDNA.

XX

XX Isoamylase; wheat; transgenic plant; starch production; food; baking;

KW pastry; packaging material; glucose; glucan; paper; pulp; adhesive;

KW textile building material; soil stabilizer; wetting agent; fertilizer;

KW plant-protection; cosmetic; flocculant; ss.

XX

OS Triticum aestivum.

XX

PH Location/Qualifiers

FT 1..2924

FT /tag= a

FT /product= "isoamylase"

FT /codon\_start= 3

FT /note= "coding sequence is interrupted by introns and the

start codon is not disclosed"

FT 1..295

FT /tag= b

FT /number= 1

FT 296..395

FT /tag= c

FT /number= 1

FT 396..1616

FT /tag= d

FT exon

FT intron

FT exon



```

FT intron /number= 2
FT 1617..2134
FT /*tag= e
FT /number= 2
FT 2135..2924
FT /*tag= f
FT /number= 3
XX
XX DE19820608-AL.
XX
XX 11-NOV-1999.
XX
XX 08-MAY-1998; 98DE-01020608.
XX
XX 08-MAY-1998; 98DE-01020608.
XX (AGRE ) HOECHST-SCHERING AGREVO GMBH.
XX
XX Loerz H, Luetticke S, Abel G;
XX
XX WPI; 2000-024509/03.
XX P-PSDB; AAY50819.
XX
XX New nucleic acid encoding isoamylase from wheat and related transgenic
XX plants producing starch with altered properties.
XX
XX Claim 1b; Page 14-15; 18pp; German.
XX
XX This invention describes a novel wheat isoamylase. Transgenic plants,
XX specifically wheat, that contain (1) are used for production of starch,
XX used particularly in foods, particularly baked and pastry goods and for
XX making packaging materials or disposable items. Starch may also be used
XX as starting materials for glucose or glucan components (e.g. for
XX fermentation or further chemical conversion); in paper and pulp
XX production; as adhesives; in textiles; in preparation of gypsum-based
XX building materials; as soil stabilizer; as wetting agent etc. in
XX fertilizer and plant-protection compositions; as binder (in
XX pharmaceuticals, cosmetics, coal briquetting and casting sand); as
XX flocculant in soil or coal slurries; as rubber and leather additives; and
XX for production of synthetic polymers, e.g. polyurethane films. Transgenic
XX plants with increased/decreased production of (1) produce starches with
XX altered physical and/or chemical properties, e.g. amylose/amylopectin
XX ratios; degree of branching; mean chain length; phosphate content;
XX gelatinization properties; gel- or film-forming properties, or starch
XX grain size or structure, e.g. easier, and less expensive, digestion by
XX enzymes. This sequence encodes the wheat isoamylase protein described in
XX the invention
XX
XX SQ Sequence 2997 BP; 803 A; 636 C; 762 G; 796 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2997
Score: 4050.00 Matches: 763
Percent Similarity: 78.34% Conservative: 0
Best Local Similarity: 78.34% Mismatches: 1
Query Match: 96.15% Indels: 211
DB: 3 Gaps: 2

US-09-674-817B-3 (1-764) x AA224492 (1-2997)

QY 1 SerGlyProAlaProArgLeuArgArgTTPArgProAsnAlaThrAlaGlyLysGlyVal 20
Dy 3 TCGGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 62
QY 21 GlyGluValCysAlaAlaValAlaGluAlaAlaThrLysValGluAspGluGluGlu 40
Dy 63 GGCAGAGTGTGCGCGCGGTGTCGAGCGCGGCGGACGAGGTAGACGACGAGGGGAGGAG 122
QY 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyCysArgValLeuAlaGly 60
Dy 123 GACGAGCGGTGGCGGAGGACAGGTACGCGCTCGGGCGGGCGGGCGGGCGGGCGGG 182
QY 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80

```

```

Dy 183 ATGCCCGCGCGCTGGGGCGGCACCGCGCTCGCCGGGGGTCAATTTTCGGCGTCTATTCC 242
QY 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97
Dy 243 GCGGAGCCACCGCGCGGGCGCTCTGCTCTTTCACGCCAGAGATCTCAAGGGGGTGGG 302
QY 97 ----- 97
Dy 303 TTGCTCCCGAGTAGAGTTATCAGCTTTGCTGCGCGCGCGCCCTTTTTCGGGGCTG 362
QY 98 -----Ala-AspArgValThrGluGluValProLe 107
Dy 363 CAATTTAAGTTTGTACTGGGGCAATGCTGCAGATAGGGTGCAGGAGGTTCCTCT 422
QY 107 uAspProLeuMetAsnArgThrGlyAsnValTIPHisValPheIleGluGluLeuHi 127
Dy 423 TGACCCCTGATGAATCGGACCGGAAACGTGTGCGATGTCTTCATCGAAGCGGAGCTGCA 482
QY 127 sAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLe 147
Dy 483 CAACATGCTTTACGGGTACAGTTTCGACGGCACCTTTGCTCTCTACCTGCGGGACACTACCT 542
QY 147 uAspValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGluTyr 167
Dy 543 TGATGTTTCCAATGCTGCTGGTGGATCCTTATGCTAAGGCAGTGATAAGCCGAGGGAGTA 602
QY 167 rGlyValProAlaArgGlyAsnAsnCysTTPProGlnMetAlaGlyMetIleProLeuPr 187
Dy 603 TGGTGTTCACGCGGTGGTAACAATGCTGGCCCTCAGATGGCTGGCATGATCCCTCTTCC 662
QY 187 oTyrSerThrPheAspTTPGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuVa 207
Dy 663 ATATAGCACGTTTGTATTGGGAAGCGACCTACCTCTAAGATATCTCTCAAAAGGACCTGGT 722
QY 207 lIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr 227
Dy 723 AATATATGAGATGACCTTGGCTGGATTTCAGAGCATGATTCAGCAATATAGAACATCC 782
QY 227 oGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnC 247
Dy 783 GGGTACTTTCTATGGAGCTGTTCGAGCTTGACTATTTCAGGAGCTTGGAGTTAATTG 842
QY 247 sIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerLys 267
Dy 843 TATTGAATTAATGCGCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCAA 902
QY 267 sMetAsnPheTTPGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSe 287
Dy 903 GATGAACCTTTTGGGGATATCTACCAATAAATCTCTTTTCCAAATGACAAAGATACATC 962
QY 287 rGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgG 307
Dy 963 AGCGGGATATAAAATCTGGGGCTGATGCCATAAATGAGTTCAAAATCTTTGTAAAGA 1022
QY 307 uAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGlu 327
Dy 1023 GGCTCACAAACGGGAATTGAGGTGATCCTGGATGTTGCTTCAACCATACAGCTGAGGG 1082
QY 327 yAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLe 347
Dy 1083 TAATGAGATGTTCCATATATATCATTTAAGGGGTGATAAATACATACATATATGCT 1142
QY 347 uAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHi 367
Dy 1143 TGCACCAAGGAGAGTATTAATACTATTCTGGCTGTGGGAATACCTTCAACTGTAATCA 1202
QY 367 sProValValArgGlnPheIleValAspCysLeuArgTyrTIPValThrGluMetHisVa 387
Dy 1203 TCCTGTGGTTCGTCAATTCATTGTAGATTGTTTAAAGATCTGGGTGACGGAATGCATGT 1262
QY 387 lAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrPaspPr 407

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Db 1263 TGATGGTTTCGTTTGATCTTCATCCATAATGACCAGAGGTTCCAGTCTGTGGATCC 1322  
 Qy 407 ovalAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuVa 427  
 Db 1323 AGTTAAGCTGTATGGAGCTCAATAGAGGTGACATGATCACACAGGACACCTCTTGT 1382  
 Qy 427 lThrProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIysLeu1 447  
 Db 1383 TACTCCACCACTTATTGACATGATCAGCAATGACCAATTCCTTGGAGGCTCAAGCTCAT 1442  
 Qy 447 eAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnVa 467  
 Db 1443 TGCTGAAGCATGGGATGAGAGGCTCTATCAAGTAGGTCAATTCCTCACTGGGAATGT 1502  
 Qy 467 lTrpSerGluTrpAsnGlyIysTyrArgAspIleValatGlnPheIleIysGlyThrAs 487  
 Db 1503 TTGTCTTGAGTGGAAATGGGAAGTACCGGACATGTGCGTCAATTCATTAAAGGCACTGA 1562  
 Qy 487 pGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAla-- 506  
 Db 1563 TGGATTTGCTGGTGGTTTTCGGAATGTCTTTGTGGAAGTCCACACTATACCAGGT-AA 1621  
 Qy 506 ----- 506  
 Db 1622 GTTGTGCAATACTGTAAATGAGTTGAGTGAATGTCACCTGGATTTTTTATATATACCA 1681  
 Qy 506 ----- 506  
 Db 1682 CATGATCATACACATCTAAATATATAACAAATCATAGTGTATGATGCTATGGCTAAG 1741  
 Qy 506 ----- 506  
 Db 1742 AAGTATTAGTGTATACACTAGTGTCTATATATAGTGTTTTAAACACCAACTTGCCTCAATGAAG 1801  
 Qy 506 ----- 506  
 Db 1802 GAACATAGGCGTTCTAGTTATCTTATTATTGTCGCGTGAATATCCACTGAAATAAT 1861  
 Qy 506 ----- 506  
 Db 1862 CCAGCCATGTCAATTTTTAGGGGGGAGAGAACTATATTGATTTGCCCTCCCTAAAGA 1921  
 Qy 506 ----- 506  
 Db 1922 AGCATCTCAGATTCATAGGTAAGTTGCTTTCTGTAAAGAAAGAAACGACTTCATA 1981  
 Qy 506 ----- 506  
 Db 1982 CTTTCTATCGGTGCTAACTTAGCTCGATGTATTTGTAAGATGAATGCCAAATTTAAT 2041  
 Qy 506 ----- 506  
 Db 2042 TGTGGATAATTGATCTGTTATTCAAAATTTCTATTGTTTCTCTAGAAATCAAACC 2101  
 Qy 507 ----- GlyGlyValArgIysPr 511  
 Db 2102 AGTAACCTGTATTGGCACTGCAACTCTCTTATTGATTAATCAGCGAGGAGAGGAAC 2161  
 Qy 511 cTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTh 531  
 Db 2162 TTGGCAGATATCAACTTGTATGTGCACATGATGGATTTACACTGCTGATTTGTAAC 2221  
 Qy 531 rTyrAsnIysIysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAs 551  
 Db 2222 ATATAATAAGAGTACAAATTTACCAATGGGAGAACACAGAGATGGAGAAATCACAA 2281  
 Qy 551 nLeuSerTrpAsnGlyGlyGluGlyGluPheAlaArgLeuSerValIysArgLeuAr 571  
 Db 2282 TCITAGCTGGAATTTGCGGGAGGAGAGAAATTCGCAAGATTTCTGTCAAAAGATTGAG 2341  
 Qy 571 gLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPh 591  
 Db 2342 GAAGAGGCAGATGGCAATTTCTTTGTTTGTCTCATGGTTTCTCAAGGAGTTTCCAATGTT 2401

Qy 591 eTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAs 611  
 Db 2402 CTCATGGGTGATGAATATGGCCACACAAAAGGGGGCAACACATACATATCTGCCATGA 2461  
 Qy 611 pSerTyrValAsnTyrPheArgTrpAspLysLysGluGlnTyrSerGluLeuHisArgPh 631  
 Db 2462 TTCCTTATGTCAATTTTTCGCTGGATATAAAGAACAAATACCTGAGTTGCACCGATT 2521  
 Qy 631 eCysLysLeuMetThrLysPheArgLysGluCysGluGlyLeuGluAspPhePr 651  
 Db 2522 CTGCTGCTCATGACAAATTCGCAAGAGTGGAGGGTCTTGGCCTTGAGGACTTTCC 2581  
 Qy 651 cThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAs 671  
 Db 2582 AACGGCCAAACGGCTGAGTGGCATGTCATCAGCTGGGAGGCTGATTTGGTCTGAGAA 2641  
 Qy 671 nSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPh 691  
 Db 2642 TAGCCGATTCGTTGCCTTTTCATGAAAGATGAAACAGACAGGCGAGATCTATGTGGCCTT 2701  
 Qy 691 eAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgArgTrpG1 711  
 Db 2702 CAACACCGCCACTTACCAGCGCTTGTGAGCTCCAGAGCGCGAGGCGCGCTGGGA 2761  
 Qy 711 uProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAspLeuProAs 731  
 Db 2762 ACCGGTGGTGACACAGGCAAGCCAGCACCATACGACTTCTCCACGACGACTTACCTGA 2821  
 Qy 731 pArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLe 751  
 Db 2822 TCGCGCTCTCACCATACACGATTCCTCGCATTTCTCTACTCCAACCTCTACCCCATGCT 2881  
 Qy 751 uSerTyrSerSerValIleLeuValLeuArgProAspVal 764  
 Db 2882 CAGCTACTCACTCGGTCATCTAGTATTGGCGCTGATGTT 2921

RESULT 2  
 AAX76375  
 ID AAX76375 standard; cDNA; 2712 BP.  
 XX  
 AC AAX76375;  
 XX  
 DT 04-AUG-1999 (first entry)  
 XX  
 DE Zea mays SU1 starch debranching enzyme encoding cDNA clone.  
 XX  
 KW Zea mays; SU1; starch debranching enzyme; maize; endosperm; corn;  
 KW bacterial isoamylase; alpha-amylase; starch hydrolytic enzyme; sugary 1;  
 KW SS.  
 XX  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..2457  
 FT /\*tag= a  
 XX  
 PN US5912413-A.  
 XX  
 PD 15-JUN-1999.  
 XX  
 PF 24-MAR-1995; 95US-00410784.  
 XX  
 PR 24-MAR-1995; 95US-00410784.  
 XX  
 PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 XX  
 PI Myers AM, James MG;  
 XX  
 DR WPI; 1999-357234/30.  
 DR P-PSDB; AAY17523.  
 XX  
 PT SU1 starch debranching enzyme.



Db	2001	CAATTATTTCGGTGGGATTAAGAGGAAGAACAAATCTCTGATTTGTACAGATTCTCGCG	2061
Qy	633	sLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAl	653
Db	2061	TCTCATGACCGAATTCGCAAAAGATGTGAATCTCTTGGCTTGAGGACTTCGCGACTTC	2120
Qy	653	aLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerAr	673
Db	2121	AGAACGGTTGAAATGGCAGCGTCATCAGCCCGGAAGCCTGACTGGTCAGAGCAAGCCG	2180
Qy	673	gPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnTh	693
Db	2181	ATTCTGTGCTTCACCATGAAGGACGAAACCAAGGCGAGATCTACTGGGCTTCAACAC	2240
Qy	693	rSerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgTrpGluProVa	713
Db	2241	CAGTCACCTTCGGGTGGTGTGTGGGCTTCCAGAGCGCTCTGGGTTCGATGGGAGCGCGT	2300
Qy	713	lValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAl	733
Db	2301	GGTGGACACCGGCAAGGAGGCACCATATGACTTCTCCAGTGGCTGCGATCGTGC	2360
Qy	733	aLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTy	753
Db	2361	TGTCAACCGTCTACCAAGTCTCTCATTTCTCAACTCCAAATCTCTATCTATGCTCAGCTA	2420
Qy	753	rSerSerValIleLeuValLeuArgProAspVal	764
Db	2421	CTCTCCATCATCTCTGATTGGCCCTGATGC	2454
RESULT 3			
AAD47816			
ID	AAD47816 standard; cDNA; 2712 BP.		
XX	AAD47816;		
AC			
DT	24-FEB-2003 (first entry)		
XX	Alternative version of maize sugary1 (SU1) cDNA.		
DE	Maize; starch debranching enzyme; sugary1; industrial application; SU1;		
XX	starch processing industry; gene; ss.		
KW	Zea mays.		
XX			
OS	Location/Qualifiers		
XX	1..2457		
PH	/*tag= a		
FT	/product= "Alternative version of SU1 protein #1"		
FT	/note= "No start codon"		
FT	/partial		
XX			
PN	US6410716-B1.		
XX			
XX	25-JUN-2002.		
PD			
XX	24-FEB-1999; 99US-00256741.		
PP			
XX	24-MAR-1995; 95US-00410784.		
PR			
XX	(IOWA ) UNIV IOWA STATE RES FOUND INC.		
PA			
XX	Myers AM, James MG;		
PI	WPI; 2002-616514/66.		
XX	P-PSDB; AAE23892.		
DR			
XX	Novel starch debranching enzyme protein sugary1 or its polypeptide		
PT	fragment useful as replacement for bacterial and fungal enzymes currently		
PT	used in starch processing industry.		
XX	Disclosure; Fig 1; 75pp; English.		
PS			
XX			

CC The invention relates to maize starch debranching enzyme, sugary1 (SUL)  
CC and nucleic acid molecules encoding such proteins. SUL sequences are used  
CC as a replacement for the bacterial and fungal enzymes currently used in  
CC the starch processing industry and as immunogens to raise antibodies  
CC against SUL. Polynucleotides of the invention are useful as markers for  
CC identification of specific corn varieties, for the development of corn  
CC varieties with starch properties tailored for specific industrial  
CC applications. The present sequence is an alternative version of maize SUL  
CC cDNA. Note: This sequence is stated to be the same as that shown as SEQ  
CC ID NO:1 (AD42890) in column 31-38 of the specification. However the  
CC sequences differ  
XX  
XX Sequence 2712 BP: 637 A: 644 C: 745 G: 686 T: 0 U: 0 Other:  
90





QY 594 lYAspGluTyrGlyHisThrIysGlyClyAsnAsnThrThrCysHisAspSerTyrV 614  
 Db 1943 GCGATGAATATGGTCAACAAAGGAGGGAAACAAATAGTACTGCTCCATGACCATATG 2002  
 QY 614 aLAsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysC 633  
 Db 2003 TCATATATTCCTGGATAGAGAGAGAAACAATCCCTGATTTGTACAGATTCTGCC 2062  
 QY 633 ysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThra 653  
 Db 2063 GTCTCATGACGGAATCCGCAAGAAATGTGAATCTCTTGGCCCTTGAGGACTTCCGCACT 2122  
 QY 653 laLysArgLeuGlnTyrPheHisGlnProGlyLysProAspTyrSerGluAsnSera 673  
 Db 2123 CAGAACGGTGAATGACAGGTTCATCAGCCCGGAGGCTGACTGTGTAGAGGCAAGCC 2182  
 QY 673 rgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnT 693  
 Db 2183 GATTCGTTGCTTCACCATGAAGACGAAACCAAGCGAGATCTACGTGGCCTTCAACA 2242  
 QY 693 hrSerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgTyrGluProV 713  
 Db 2243 CCAGTCACTTCGCGTGGTGTGGGCTTCCAGAGCGCTCTGGGTTCGATGGAGCGCG 2302  
 QY 713 alValAspThrGlyLysProAlaProAlaProTyrAspPheLeuThrAspLeuProAspArg 733  
 Db 2303 TGGTGGACACCGGCAAGGAGGACCATATGACTTCTCACCAGATGCCCTGCCAGATCGT 2362  
 QY 733 laLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerT 753  
 Db 2363 CTGTCAACGCTACCACTCTCTCATTCCTCAACTCCAATCTCTATCTATCTATGCTCAGCT 2422  
 QY 753 yrSerSerValIleLeuValLeuArgProAspVal 764  
 Db 2423 ACTCCTCATCATCTCTGTATTGGCCCTGATGTC 2457  
 RESULT 5  
 ID AAX27061 standard; DNA; 2706 BP.  
 XX  
 AC AAX27061;  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE S. tuberosum isoamylase clone 15 coding sequence.  
 XX  
 DE Isoamylase clone; potato; branched polysaccharide synthesis; amylopectin;  
 KW starch modification; debranching activity; ss.  
 XX  
 OS Solanum tuberosum.  
 XX  
 PN WO9906575-A1.  
 XX  
 PD 11-FEB-1999.  
 XX  
 PF 30-JUL-1998; 98WO-05002280.  
 XX  
 PR 31-JUL-1997; 97GB-00016185.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Edwards EA, Smith AM, Martin CR, Bustos Guillen R;  
 XX  
 DR WPI; 1999-153803/13.  
 DR P-PSDB; AAY00869.  
 XX  
 PT New nucleic acid from potato encoding starch debranching enzyme with  
 PT isoamylase activity - and related vectors, transformed cells and plants,  
 PT proteins and antibodies, used to generate starch with altered properties,  
 PT for use in foods, as thickeners etc.  
 XX  
 PS Claim 3; Fig 2; 78pp; English.

XX  
 CC This sequence encodes a Solanum tuberosum isoamylase of the invention.  
 CC Fragments of the isoamylase coding sequence are used to identify and  
 CC clone isoamylases from other plant species, by standard hybridisation or  
 CC amplification methods. Expression of the isoamylase DNA in host cells is  
 CC used to produce the isoamylase which is used: (i) to raise antibodies  
 CC (Ab) for identification, isolation and localisation of isoamylases; and  
 CC (ii) for synthesis of branched polysaccharides. The DNA, proteins and Ab  
 CC (or related peptides) are used to alter the quality and quantity of  
 CC polysaccharides in a host cells, specifically to alter branching in  
 CC amylopectin. The modified starches produced are useful in human or animal  
 CC foods; as biodegradable plastic; as food or paint thickener; in starch-  
 CC coated films, paper and textiles; in mining explosives; in  
 CC pharmaceuticals and glues. Manipulation of debranching activity in a  
 CC plant allows control of starch properties, e.g. increased gel strength;  
 CC formation of paste rather than gel, changed physical characteristics etc  
 XX  
 SQ Sequence 2706 BP; 797 A; 492 C; 624 G; 792 T; 0 U; 1 Other;  
 Alignment Scores:  
 Pred. No.: 6,54e-279 Length: 2706  
 Score: 3029.00 Matches: 546  
 Percent Similarity: 81.57% Conservative: 78  
 Best Local Similarity: 71.37% Mismatches: 113  
 Query Match: 71.91% Indels: 28  
 DB: 2 Gaps: 7  
 US-09-674-817B-3 (1-764) x AAX27061 (1-2706)  
 QY 10 TrpArgPro-----AsnAlaThrAlaGlyLysGlyValGlyGluVal 23  
 Db 178 TGGAGAAAATCGAGGTCTTCAGTGGTTAATGCTGCTGTATGATGGACGTGGGTGTG 237  
 QY 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluGluAspGluPro 43  
 Db 238 -----GTGAAGACTGGCGTACTCGGTGGTGGTGAG-----AAGCGG 276  
 QY 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArg-----ValLeuAlaGlyMet 61  
 Db 277 ACGACGGAA-----CGATGCTGTTTGGAGGTTTATCAGGGAAG 315  
 QY 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGly 81  
 Db 316 CCATTGCGGTTTGGTGTCTACTGCGACAGATGGTGTGAATTCGCTGTTTTCAGG 375  
 QY 82 GlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101  
 Db 376 AATGCTACAGCTGCTACTCTTTGCTTGCATCACTCTTTCCGATTACCTGAGAAGAGAGTG 435  
 QY 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTyrHisValPhe 121  
 Db 436 ACCAGCAAAATTTCCCTGGATCCTCTAGCTAAATAAACTGGAGATGTATGCGATGTGTC 495  
 QY 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141  
 Db 496 CTTAAGGGAGATTTTGAGATATGCTATATGGCTACAAATTCATGGAAATCTGCTCT 555  
 QY 142 HisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaVal 161  
 Db 556 GAAGAAGGACACTACTTTGACTCTTCGACATAGTGTGGATCTTATGCAAGGCTATA 615  
 QY 162 IleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTyrProGlnMetAla 181  
 Db 616 GTAACGACGAGGAGATATGTTGTTATAGGCCACAGAGATGTTGTTGGCCCCCAATGGCT 675  
 QY 182 GlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyr 201  
 Db 676 GGCATGTGCTCTCTGCTTCTGATCAGTTTGAITGGGAGGAGATCTTACCACTCAAGTTT 735  
 QY 202 ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSer 221  
 Db 736 CCACGAGAGATCTTGTAAATGATGATGTTGCTGGGTTTACTATCATGAGTCG 795





XX Disclosure; Fig 11; 7app; English.

XX This sequence represents the original isolated clone encoding a Solanum  
 CC tuberosum isomylase of the invention. Fragments of the isomylase coding  
 CC sequence are used to identify and clone isomylases from other plant  
 CC species, by standard hybridisation or amplification methods. Expression  
 CC of the isomylase DNA in host cells is used to produce the isomylase  
 CC which is used: (i) to raise antibodies (Ab) (for identification,  
 CC isolation and localisation of isomylases); and (ii) for synthesis of  
 CC branched polysaccharides. The DNA, proteins and Ab (or related peptides)  
 CC are used to alter the quality and quantity of polysaccharides in a host  
 CC cells, specifically to alter branching in amylopectin. The modified  
 CC starches produced are useful in human or animal foods; as biodegradable  
 CC plastic; as food or paint thickener; in starch-coated films, paper and  
 CC textiles; in mining explosives; in pharmaceuticals and glues.  
 CC Manipulation of debranching activity in a plant allows control of starch  
 CC properties, e.g. increased gel strength; formation of paste rather than  
 CC gel, changed physical characteristics etc

XX Sequence 2806 BP; 818 A; 523 C; 654 G; 807 T; 0 U; 4 Other;

## Alignment Scores:

Pred. No.: 9,31e-269 Length: 2806  
 Score: 2923.00 Matches: 538  
 Percent Similarity: 80.23% Conservative: 79  
 Best Local Similarity: 69.96% Mismatches: 119  
 Query Match: 69.40% Indels: 33  
 DB: 2 Gaps: 9

US-09-674-817B-3 (1-764) x AAX27066 (1-2806)

Qy 10 TrpArgPro-----AsnAlaThrAlaGlyLysGlyValGluVal 23  
 Db 241 TGGAGAAATCGAGGCTTCAGTGGTTAATGCTGCTTGTATAGTGGACGTGGAGGTG 300  
 Qy 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGluAspGluPro 43  
 Db 301 -----GTGAAGACTGGCGGTACTGCGGTGGTGGAG-----AAGCCG 339  
 Qy 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgVal-----LeuAlaGlyMet 61  
 Db 340 ACGACGAA-----CGATGTCGTTGAGGTTTTCAGGGAAAG 378  
 Qy 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGly 81  
 Db 379 CCATTGCGGTTTGGTGTCTACTGCGACAGATGGTGGTGAATTCGCTGTTTTCAGGA 438  
 Qy 82 GlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101  
 Db 439 AATGCTACAGCTGCTACTCTTCTGCTGATCATCTCTTCCGATTTACTGAGAGAGAGTG 498  
 Qy 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPhe 121  
 Db 499 ACCGAGCAAAATTTCTCGGATCCTCTAGCTAATAAATACTGGAGATGTATGGCATGTGTT 558  
 Qy 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141  
 Db 559 CTTAAGGGAGATTTGAGATATGCTATATGGCTACAAATTTGATGGAAATTTCTGCTCT 618  
 Qy 142 HisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaVal 161  
 Db 619 GAAGAAGGACACTACTTTGACTCTTCGACATAGTGTGGATCTTATGCCAAGGCTATA 678  
 Qy 162 IleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAla 181  
 Db 679 GTAAGCAGAGAGAGAATATGTTGATTAGGGCCAGAGATGATTGTCGCCCAATGGCT 738  
 Qy 182 GlyMetIleProLeuProTyr---SerThrPheAspTyrGluGlyAspLeuProLeuArg 200  
 Db 739 GGCATGTTACCTTCTGCTCTGATCAGTTTGTATTTGGAGAGAGATCTACCACTGGAA 798  
 Qy 201 --TyrProGlnLysAspLeuVal-IleTyrGluMetHisLeuArgGlyPheThrLysHis 219

Db 799 GTTTCACACAGAGATCTTCTTATCNATGAAATGCATGTTCTGCTGGTTTACTATCAT 858  
 Qy 220 AspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyr 239  
 Db 859 GAGTCGAGTGAACAACAATAATCTCTGGTACTTACCTGGTGTGGGAGAACTTGATCAC 918  
 Qy 240 LeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeu 259  
 Db 919 TTGAAGAGACTTGGTGTCACTGTATAGAGTATAGCCCTGTACAGAGTTCAATGACGTG 978  
 Qy 260 GluTyrSerThrSerSerSer-----LysMetAsnPheTrpGlyTyrSer 274  
 Db 979 GAGTACTATATGTTAACTCTGTATGGCGACACAAAGTTTAACTTTTGGGGCTATCT 1038  
 Qy 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294  
 Db 1039 ACTGTCAATTTCTTTTCTCCAAATGGGAGATACTCATCTGCTGCTTAAGTAATTTGGCG 1098  
 Qy 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314  
 Db 1099 CTCGGTGCATAAACAAGATTTAAGTATCTTGTCAAGGAAGCACATAAACCGTGAATCGAG 1158  
 Qy 315 ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu 334  
 Db 1159 GTTATCATGGATGTTGTTTTCATACACACTGCTGAAGGAATGAAATGGTCCCATACTA 1218  
 Qy 335 SerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyr 354  
 Db 1219 TCATTTAGAGCAATGACACAGTGTGTTTATACGCTAGCTCTCAAGGGTGAATTTTAC 1278  
 Qy 355 AsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIle 374  
 Db 1279 AACTACTCAGATGTGAATATACCTTCAACTGTAAATATCCCATGTACGTCAATTTATA 1338  
 Qy 375 ValAspCysLeuAspTyrTyrValThrGluMetHisValAspGlyPheArgPheAspLeu 394  
 Db 1339 GTG---ATGCTGAGATATGGTTTACCGAATGACAGTACATGGCTTCCGCTTGATCTT 1395  
 Qy 395 AlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaPro 414  
 Db 1396 GCTTCTATCTCTACAGAAGTAGCAGCTCGTGAATGCTGTAAATGCTCTATGAAATTC 1455  
 Qy 415 IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMet 434  
 Db 1456 ATTGACGTGACGTGATCACACAGGACCTCTCTCAAGCCACCATTTGATGATG 1515  
 Qy 435 IleSerAsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly 454  
 Db 1516 ATTAGCAATGATCCAATACTTCTGAGTAAAGCTTATAGCTGAAGCATGGGATTGTGA 1575  
 Qy 455 GlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLys 474  
 Db 1576 GGCCTTTACCAAGTGGCATGTTTCCGCACCTGGGGTATCTGTCGGAGTGAACGGAAG 1635  
 Qy 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAla 494  
 Db 1636 TACGCTGACATGGTACGGCAGTTCATCAAGGCATCTGATGGTTTCTGGGGCTTTTGT 1695  
 Qy 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSer 514  
 Db 1696 GAATGCTCTTGTGAAGCCCAATCTATACAGAAGGAGAGAAACCATCGAACAGT 1755  
 Qy 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534  
 Db 1756 ATAAATTCGTGTGTGCCAGATGGTTTACTTTGCTGATTTAGTGACATACACAAT 1815  
 Qy 535 LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrp 554  
 Db 1816 AAACACAATTTGGCAATGGAGAGACACAACAAGACGGGAGATCAATAATAGTTGG 1875  
 Qy 555 AsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuAspGlyArgGln 574

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Db 1876 AATTGTCGTGAGGAGAGAAATTTGCAAGATATCTTTGTGAAGAAATTTGAGGAAAAACACAA 1935
Qy MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594
Db 1936 ATGGGAACTTCTTCCTCTGCTTATGTTTCCCAAGGTGTTCCCATGATATATATGGGC 1995
Qy 595 AspGluTyrGlyHisThrLysGlyGlyValAsnAsnThrTyrCysHisAspSerTyrVal 614
Db 1996 GATGAATATGTCACATTAAGGGAGGAAACAAACACACGTATTGCCATGATAATATATT 2055
Qy 615 AsnTyrPheArgTTPAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys 633
Db 2056 AATTACTTCGTTGGGATAAGAGATGAATCTTCATCTGATTTTTTGAGATTTTGGGC 2115
Qy 634 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGlyLeuGluAspPheProThrAla 653
Db 2116 CTCATGACCAAAATTCGCCATGAATGAATCACTGGGATTAGATGGTTTCCCTACAGCA 2175
Qy 654 LysArgLeuGlnTTPHisGlyHisGlnProGlyLysProAspTTPSerGluAsnSerArg 673
Db 2176 GAAAGGTGCAATGGCATGGTTCACACTCTTAGBACTCCAGATTGGTCTGAACAAGTCGA 2235
Qy 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnThr 693
Db 2236 TTCGTTGCATTCACACTGCTGCGACAAAGTGAAGGGAGAACTATATATTGCTTTAACGCC 2295
Qy 694 SerHisLeuProAlaValGluLeuProGluArgAlaGlyArgArgTTPGluProVal 713
Db 2296 AGCCATTGCTTGAACATTTACACTTCCAGATAGCGCTGGTTATAGATGGCAGCGCTTT 2355
Qy 714 ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla 733
Db 2356 GTGCACACAGCAAAACAGCACCATTTGACTTCTTGACAGCAGCTTCCTGAGAGAGAG 2415
Qy 734 LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr 753
Db 2416 ACAGCAGCAAAACAAATATTTCTATTTTCGACGCGAACCAGTATCCGATGCTCAGTTAT 2475
Qy 754 SerSerValIleLeuValLeu 760
Db 2476 TCATCCATTTCTTTTACTA 2496

RESULT 7
AAX34654
ID AAX34654 standard; cDNA; 1706 BP.
XX
AC AAX34654;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Partial cDNA for hexaploid wheat DBE.
XX
KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS;
KW starch branching enzyme; starch soluble synthase; debranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein I; bacterial isomylase; glycogen synthase;
KW wSBE I-D4 gene; ss.
XX
OS Aegilops tauschii.
XX
PH Location/Qualifiers
FT CDS
FT 1..1704
FT /*tag= a
FT /note= "partial DBE; the att and stop codons are not
FT indicated"
XX
PN W09914314-A1.
XX
PD 25-MAR-1999.
XX
PF 11-SEP-1998; 98WO-AU000743.
XX

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PR 12-SEP-1997; 97AU-00009108.
PR 20-MAR-1998; 98AU-00002509.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU ) UNIV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
PI Li Z, Morell M, Rahman S;
XX
DR WPI; 1999-229525/19.
DR P-PSDB; AAY06918.
XX
PT New isolated cereal plant enzyme genes used for, e.g. expression of
PT antisense sequences of granule bound synthase.
XX
PS Claim 47; Page 100-102; 171pp; English.
XX
CC The invention relates to a novel enzyme of starch biosynthetic pathway in
CC a cereal plant, where the enzyme is selected from starch branching enzyme
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of
CC rice or maize. The methods and products can be used for targeting
CC expression specifically to the endosperm of the seeds of cereal plants
CC such as wheat or barley. They can be used for the expression of e.g.
CC antisense sequences of granule-bound synthase (GBS), SBE II, low mol.
CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial
CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be
CC used for modifying the characteristics of starch produced by a plant. The
CC present sequence represents the wheat DBE partial cDNA sequence. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1706 BP; 467 A; 355 C; 415 G; 469 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 1.37e-268 Length: 1706
Score: 2918.00 Matches: 525
Percent Similarity: 99.25% Conservative: 3
Best Local Similarity: 98.68% Mismatches: 4
Query Match: 69.28% Indels: 0
DB: 2 Gaps: 0

US-09-674-817B-3 (1-764) x AAX34654 (1-1706)

Qy 233 AlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetPro 252
Db 1 GCTGTGTCGAGCTTGACTATTGAGGAGCTTGAGTTAATTGTTGTAATTAATGCC 60
Qy 253 CysHisGluPheAsnGluLeuGluTyrSerThrSerSerSerLysMetAsnPheTTPgly 272
Db 61 TGCCATGAGTTCACGAGCTGGAGTACTCAACCTCTTCTCCAGATGAACCTTTTGGGGA 120
Qy 273 TyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyIleLysAsn 292
Db 121 TATTTCCATTAATATCTTTTCCACATGACGAGATACATCATCAGCGGGGNTAATAAAC 180
Qy 293 CysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGly 312
Db 181 TGTGGCGGTGATGCCATAAATGAGTTCAAACTTTTGTAAAGAGAGCGCTCACAAACGGGA 240
Qy 313 IleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyPro 332
Db 241 ATTGAGGTGATCTCGATGTTGCTTCAACCATACAGCTGAGGGTATAGAGTATGTTCA 300
Qy 333 IleLeuSerPheLysGlyValAspAsnThrTyrTyrMetLeuAlaProLysGlyGlu 352
Db 301 ATATTATCATTTAGGGGGTGCATATACTACTATATGTTGTCACCAAGGAGAG 360
Qy 353 PheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGln 372
Db 361 TTTTATAACTATTCTGGCTGGGAATACCTTCAACTGATTAATCATCTGTTGTTGCTCAA 420
Qy 373 PheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPhe 392

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Db 421 TTCTAGTATTGTTTAAAGTACTGGGTGATGGAATGATGTTGATGTTTTCGTTTT 480  
 Qy 393 AspleualaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTrpGly 412  
 Db 481 GATCTTCATCCATAATGACAGAGGTTCAGTCTGGGATCCAGTTAACGGTGTATGGA 540  
 Qy 413 AlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIle 432  
 Db 541 GCTCCANTAGAGGTGACATGATCACACAGGACACCTCTTGTACTCCACCACCTATT 600  
 Qy 433 AspMetIleSerAsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAsp 452  
 Db 601 GACATGATCAGCAATGACCAATTTCTGGAGGGCTCAAGCTCATGCTGAAGCATGGAT 660  
 Qy 453 AlaGlyGlyLeuTrpGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsn 472  
 Db 661 GCAGAGGCTCTATCAAGTAGGTCAATTCCTCCTCAGTGGAAATGTTTGGTCTGAGTGAAT 720  
 Qy 473 GlyLysTrpArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGly 492  
 Db 721 GGGAGGTACCGGACATTTGTGGCAATTCATTAAGGCACCTGATGCAATTTGCTGGTGGT 780  
 Qy 493 PheAlaGluCysLeuCysGlySerProHisLeuTrpGlnAlaGlyArgLysProTrp 512  
 Db 781 TTTCCCGAATGCTTTTGTGAAGTCCACACCTATACAGGCGAGGAGGAAACCTTGG 840  
 Qy 513 HisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTrp 532  
 Db 841 CACAGTATCAACTTTGTATGTGCACATGATGGATTTACACTGGGTGATTTGGTAACATAT 900  
 Qy 533 AsnLysLysTrpAsnLeuProAsnGlyGluAsnArgAspGlyGluAsnHisAsnLeu 552  
 Db 901 AATAACAAGTACATTTTACCAATGGGGAGAACAAATAGAGATGGAGAAATCAATCTT 960  
 Qy 553 SerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLys 572  
 Db 961 AGCTGGATTTGTGGGAGGAGGAGATTCGACAGATTGTCTCAAAAGATTGAGGAAG 1020  
 Qy 573 ArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTrp 592  
 Db 1021 AGGCAGATGGCAATTTCTTTGTTGTCTCATGCTTCTCAAGGAGTTCCAATGTTTAC 1080  
 Qy 593 MetGlyAspGluTrpGlyHisThrLysGlyGlyAsnAsnThrTrpCysHisAspSer 612  
 Db 1081 ATGGCGCATGATATGCCACACAAAGGGGGCAACAACTATCTGCTGCTGCTGCTGCT 1140  
 Qy 613 TyrValAsnTrpPheArgTrpAspLysLysGluGlnTrpSerGluLeuHisArgPheCys 632  
 Db 1141 TATGTCAATTTATTCGCTGGGATAAAAAAGAACAAATCTCTCACTTGCACAGATTCTGC 1200  
 Qy 633 CysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThr 552  
 Db 1201 TGCTCTATGACCAATTTCCGCAAGGAGTGGAGGGTCTTGGCCTTGAGGACITTTCCACG 1260  
 Qy 653 AlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSer 672  
 Db 1261 GCCGAACGGTGCAGTGGCATGGTCTACCTGGGAGGCTGATTTGCTGAGATAGC 1320  
 Qy 673 ArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTrpValAlaPheAsn 692  
 Db 1321 CGATTCGCTGCTTTTCCATGAAGATGAAAGACAGCGCGAGATCTATGTGGCTTCAAC 1380  
 Qy 693 ThrSerHisLeuProAlaValGluLeuProGluArgAlaGlyArgTrpGluPro 712  
 Db 1381 ACCAGCCACTTACCGGCGCTTGTGTAGTCTCCAGAGCGCGCGCGGTGGAGACCG 1440  
 Qy 713 ValValAspThrGlyLysProAlaProTrpAspPheLeuThrAspAspLeuProAspArg 732  
 Db 1441 GTGGTGACACAGGCAAGCAGCACCATATGACTTCTCCTCACCAGCACTTACCTGATCGC 1500  
 Qy 733 AlaLeuThrIleHisGlnPheSerHisPheLeuTrpSerAsnLeuTrpProMetLeuSer 752

Db 1501 GCTCTCACCATAACACCACTTCTCTCAATTCCTCACTCAACCTCTACCCCATGCTCAGC 1560  
 Qy 753 TyrSerSerValIleLeuValLeuArgProAspVal 764  
 Db 1561 TACTCATCGGTCACTCTAGTATTGGCCCTGATGTT 1596  
 RESULT 8  
 ABZ12413  
 ID ABZ12413 standard; DNA; 2352 Bp.  
 XX ABZ12413;  
 AC ABZ12413;  
 XX 21-JAN-2003 (first entry)  
 DT 21-JAN-2003 (first entry)  
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 218.  
 DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
 KW Arabidopsis thaliana;  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX WO200216655-A2.  
 PN 28-FEB-2002.  
 XX 24-AUG-2001; 2001WO-US026685.  
 PF 24-AUG-2001; 2000US-0227866P.  
 PR 26-JAN-2001; 2001US-0264647P.  
 PR 22-JUN-2001; 2001US-0300111P.  
 XX (SCEI ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX Harper JF, Kreps J, Wang X, Zhu T;  
 PI WPI; 2002-304127/34.  
 DR Identifying a stress condition to which a plant cell has been exposed and  
 PT producing plants with increased tolerance to these abiotic stresses.  
 XX Claim 144; SEQ ID NO 218; 577pp + Sequence Listing; English.  
 CC The invention relates to identifying a stress condition to which a plant  
 CC cell has been exposed, comprising: (a) contacting nucleic acid  
 CC representative of expressed polynucleotides in the plant cell with an  
 CC array or probes representative of the plant cell genome; and (b) the  
 CC detecting a profile of expressed polynucleotides in the plant cell  
 CC characteristic of a stress response. The method is useful in the  
 CC production of transgenic plants, cells and seeds and in producing plants  
 CC with increased tolerance to abiotic stress. The present sequence is that  
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
 CC in methods of the invention. Note: The sequence data for this patent is  
 CC not represented in the printed specification but is based on sequence  
 CC information supplied to Derwent by the European Patent Office  
 XX SQ Sequence 2352 Bp; 664 A; 475 C; 545 G; 668 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.07e-266 Length: 2352  
 Score: 2895.50 Matches: 518  
 Percent Similarity: 81.08% Conservative: 82  
 Best Local Similarity: 70.00% Mismatches: 127  
 Query Match: 68.74% Indels: 14  
 DB: 6 Gaps: 4  
 US-09-674-817B-3 (1-764) x ABZ12413 (1-2352)  
 Qy 29 GluAlaAlaThrLysValGluAspGluGlyGluAspGluProValAlaGluAspArg 48  
 Db 140 GAAGAAGCACGAAGCT-GAAATATCGCGTAGTAGAGAACTCTTAATCAGATAGA 198  
 Qy 49 TyrAlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 68

Db 199 TTTTATCTCCGAT-----GGACTTCTCTCTCCATTCGACCCACC 240  
Qy 69 AlaLeuAlaGlyValAsnPheAlaValTyrSerGlyValAlaThrAlaAlaLeu 88  
Db 241 GTGAGACACGCGGTCATTTCTCTGTTTACTCTACAACTCCGTTCCGCTACCATC 300  
Qy 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAsp 108  
Db 301 TGCTTGATTTCTCTCTCCGATCTCCGTCAGAACAAAGTCACGAGGAGATTGAGCTTGAT 360  
Qy 109 ProLeuMetAsnArgThrGlyAsnValTyrHisValPheIleGluGlyLeuHisAsn 128  
Db 361 CCATCAAGGAATAGAACTGGCCATGTTGGCATGTGTTTGAGAGAGATTTCAAAGAT 420  
Qy 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148  
Db 421 ATGCTGATGTTATAGATTGATGGCAAGTTTCTCTGGAAGAAGTCAATTATTATGAT 480  
Qy 149 ValSerAsnValValAlaAspProTyrAlaLysAlaValIleSerArgGlyGluTyrGly 168  
Db 481 TCCTCCCAACATTTATTGGATCCTTAGCAAGGCAATATAAGCAGAGATGAGTTTGA 540  
Qy 169 ValProAlaArgGlyAsnAsnCysTyrProGluMetAlaGlyMetIleProLeuProTyr 188  
Db 541 GTTTTGGGACCTGATGATATTGTTGGCTCAATGGCGTATGTGACCCACTCGTAG 600  
Qy 189 SerThrPheAspThrGluGlyAspLeuProLeuArgTyrProGluLysAspLeuValIle 208  
Db 601 GAAGAGTTTGAATGGGAAGGGATATGCATCTGAAGCTCCACAGAAAGATCTTGTATA 660  
Qy 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228  
Db 661 TATGAATGCGATGCGGAGTTTACAAAGCATGAGTCTAGTAAATTTGAAATTCCTTGGC 720  
Qy 229 ThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIle 248  
Db 721 ACATACCAGGCTGTTGCAGAAAGCTTGACCAATTTGAAGGAGCTTGGGATAAATTGTATA 780  
Qy 249 GluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSer----- 266  
Db 781 GAATTAATGCCATGTCAGAGTTTAATGAGCTGGAGTATTACAGCTACATAGATTTTG 840  
Qy 267 -----LysMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSerProMetThr 283  
Db 841 GGAGACCACAGGTAATTTTGGGTTACTCTACCATTTGGTCTCTCCGCCATGATC 900  
Qy 284 ArgTyrThrSerGlyGlyLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303  
Db 901 AGATACGCATCAGCAAGCTCTAACAAATTTTGGCTGGACGCCATAAATGAATTCAAAAT 960  
Qy 304 PheValArgGluAlaHisLysAtsGlyIleGluValIleLeuAspValValPheAsnHis 323  
Db 961 CTGTTAAGAGGCACTAAACGAGGAAATGAGGTAATCATGATGCTCTTGAACAC 1020  
Qy 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343  
Db 1021 ACAGCCGAAGGAATGAAAAAGGCCCATTTTCTCATTTAGAGAGTTGATAACAGTGC 1080  
Qy 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363  
Db 1081 TATTACATGCTGTCTCAAAAGGGGAGTTCTTAATTAATTATTACGCTGTGTAATACATC 1140  
Qy 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTyrPheValThr 383  
Db 1141 AACTGCAATCATCTGTGGTGGTCAATTCATATTGGATTGGCTGAGATATTGGGTACA 1200  
Qy 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403  
Db 1201 GAAATGATGTTGACGCGCTTCGCTTTGATCTTGGTTCAATCATGTCAAGGACGACGAGC 1260  
Qy 404 LeuTrpAspProValAsnValTyrGlyValAlaProIleGluGlyAspMetIleThrThrGly 423  
Db 1261 CTTTGGGATGCAGCAATGTTTACGGGCTGATGTAGAAAGTGACTGCTGCACAACTGGT 1320

Qy 424 ThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIleLeuGlyGly 443  
Db 1321 ACTCTATTAGCTGCCCTCCAGTAATTCACATGATAAGTAATGATCCAACTACTCCGCGT 1380  
Qy 444 ValLysLeuIleAlaGluAlaTyrAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463  
Db 1381 GTTAGCTTAATAGCTGAAGCATGGGATGGCGGTGGCTGTACCAAGTTGGCATGTTTCCA 1440  
Qy 464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483  
Db 1441 CACTGGGATATTGGTCTGAGTGGATGGAAATGGAAATTTCCGGATGTTGTGAGACAGTTCATA 1500  
Qy 484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503  
Db 1501 AAAGCACCGATGGCTTTTCTGCTGCTTTCTGCTGAATGCTCTGTGGAAGCCCAATCTG 1560  
Qy 504 TyrGlnAlaGlyGlyValGlyProTyrHisSerIleAsnPheValCysAlaHisAspGly 523  
Db 1561 TACCAG----GGAGGTAGGAACCTTTGGCAGCAGCATCAATTTATATGTGCGCATGATGCT 1617  
Qy 524 PheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsn 543  
Db 1618 TTTACGTTGGCAGATTTAGTAATTAACAATAAGAAATAACTTGGCAATGGGAGAGAG 1677  
Qy 544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlyGluPheAla 563  
Db 1678 AATAATGATGAGAGAAATCAAAATTTACAGCTGGAACTGTGGAGAGAGGAGACTTTCCG 1737  
Qy 564 ArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMet 583  
Db 1738 AGTATCTCGTCAAGAGACTAAGGAACAGCAGATGCGGAATTTCTTTGTTCCCTCATG 1797  
Qy 584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603  
Db 1798 GTTTCCTCCAGGTGCTCCCAATGATTTTACATGGAGATGAATATGGCCATCTAAAGGGGA 1857  
Qy 604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGlu 623  
Db 1858 AACAAACACAGTATGTCATGACAACTATATGAACTATTTTCGGTGGGATAAAGGAA 1917  
Qy 624 Gln---TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642  
Db 1918 GAAGCACATCTGACTTCTTCAGATTTCTCCGCTATTTCTTATCAAGTTTTCGTGATGAATGT 1977  
Qy 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662  
Db 1978 GAATCACTGGCTTGAATGATTTCCCAACAGCAAGCGTCTGCAGTGGCATGTTCTTGTCT 2037  
Qy 663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682  
Db 2038 CCTGAGATCCCAAAATTTGGTCTGAAACAAAGTCGATTTGTTGCAATTTTCACTGCTCATCT 2097  
Qy 683 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702  
Db 2098 GTGAAGAAGAAATCTATGTGCGCTTCAACACCATCTCAATTTAGCCACACTGTTTTCGCTA 2157  
Qy 703 ProGluAtsGlyAlaGlyArgTyrGluProValValAspThrGlyLysProAlaProTyr 722  
Db 2158 CCGAATAGCCAGGATACCGATGGAGGCAATTTGTAGACAGCAGCAACCGACCTTAC 2217  
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742  
Db 2218 GACTGCATAAACCCGATCTCCAGAGAGAGAAACGGCGATGAAGCAGTATAGGCACATC 2277  
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762  
Db 2278 TTAGATGCAATGATGTACCAATGCTCAGTTACTCATCATCTCTCTCTTCTTTCACCA 2337  
RESULT 9  
ADA67900  
ID ADA67900 standard; DNA; 2352 BP.  
XX







301 PhylLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal 320  
 419 TTTAAGTATCTTGTCAAGGAGACACATAAAGCTGGATCGAGTTATCATGGATGTGT 478  
 321 PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp 340  
 479 TTCAATCACACTGCTGAAGAAATGAAATGGTCCCATACTATCATTTAGAGCAATGAC 538  
 341 AsnThrThrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly 360  
 539 AACAGTGTGTTTATACGCTAGCTCCCTAAGGAGAAATTTTACAACTACTCAGATGTGA 598  
 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380  
 599 AATACCTTCAACTCTAATAATCCCATTTGATGCAATTTATAGTGGATGCTTGATAT 658  
 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400  
 659 TGGTTTACCGAAATGCCAGTAGATGGCTTCGGCTTTGATCTTCTTCTATCTTACAAGA 718  
 401 GlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420  
 719 AGTAGAGCTCGTGAATGCTGAATGCTATGGAATTCATTCAGCTGACATGATC 778  
 421 ThrThrGlyThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIle 440  
 779 ACCACAGGCATCTCTCACAAAGCCCACTTGAATGATATGATGATGATGATGATGAT 838  
 441 LeuGlyGlyValLysLeuIleAlaGluAlaTyrAspAlaGlyGlyLeuTyrGlnValGly 460  
 839 CTAGTGGATGAAGCTTATAGCTCAAGCATGGATGCTGGAGCCCTTACCAAGTTGGC 898  
 461 GlnPheProHisTyrAsnValTyrSerGluTyrAsnGlyLysTyrArgAspIleValArg 480  
 899 ATGTTTCGGCACTGGGTATCTGCTGGAGTGAACCGAAAGTACCGTGACATGGTACGT 958  
 481 GlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySer 500  
 959 CAGTTTCATCAAGGACATGATGGTGTCTGGGGCTTTTCTGAAATGCTTGTGGAGC 1018  
 501 ProHisLeuTyrGlnAlaGlyGlyValArgLysProTyrHisSerIleAsnPheValCysAla 520  
 1019 CCAATCTATACACAGAGGAGGAGGAGAAACCACTGGAACAGTATAAATTCGTGTGTGC 1078  
 521 HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn 540  
 1079 CACGATGGTTTACTTTGGCTGATTTTATGATACATACCAATTAACACAAATTTGGCAAT 1138  
 541 GlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrAsnCysGlyGluGly 560  
 1139 GGAGAGGACAAAGATGGGAGAAATCACATAATAGTTGGATTTGGCGAGGAGGA 1198  
 561 GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal 580  
 1199 GAATTTGCAATATCTTTGTGAAGAAATGAGGAAAGACAAATTCGGAATCTTCTCCTC 1258  
 581 CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr 600  
 1259 TGCCTTATGGTTTCCCAAGGTGTTCCCATGATATATATGGTGGATGATATGATGAT 1318  
 601 LysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAsp 620  
 1319 AAGGAGGAAACAAACACATGATTCGATGACATATATTAATTAATTAATTAATTAAT 1378  
 621 LysLys---GluGlnTyrSerGluLeuHisArgPheCysLeuMetThrLysPheArg 639  
 1379 AAGAGAGATGAATCTTCATCTGATTTTGGAGATTTTGGCGCTCATGACAAATTCGCG 1438  
 640 LysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnThrHis 659  
 1439 CATGAATGTGAATCACTGGGATTAGATGGTTTCCTACACAGCAAGGCTGCAATGGCAT 1498

QY 660 GlyHisGlnProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPheSerMet 679  
 DB 1499 GGTCACTCTCTAGAACTCCAGATTGGTCTGAAACAAAGTCGATTGCTGATTACACTG 1558  
 QY 680 LysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaVal 699  
 DB 1559 GTCGACAAAGTGAAGGAGAACTATATATGCTTTTAAAGCCAGCCATTTGCCCTGTAAAG 1618  
 QY 700 ValGluLeuProGluArgAlaGlyArgTyrGluProValValAspThrGlyLysPro 719  
 DB 1619 ATTACACTTCCAGAAAGCGCTGTTATAGATGGCAGCGTTTGGACACAGGCAACCA 1678  
 QY 720 AlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPhe 739  
 DB 1679 GCACCAATTTGACTTCTGACAGACGATGTTCTCTGAGAGAGACAGCAGCAACCAATAT 1738  
 QY 740 SerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuVal 759  
 DB 1739 TCTCATTTCTGGAGCGCAACCACTATCCGATGCTCAGTTATTCATTCATTCATTT 1798  
 QY 760 Leu 760  
 DB 1799 CTA 1801  
 RESULT 11  
 AAX34655  
 ID AAX34655 standard; DNA; 9289 BP.  
 AC AAX34655;  
 DT 17-OCT-2003 (revised)  
 DT 05-JUL-1999 (first entry)  
 DE Hexaploid wheat DBE genomic sequence.  
 KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;  
 KW starch branching enzyme; starch soluble synthase; debranching enzyme;  
 KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;  
 KW grain softness protein 1; bacterial isomylase; glycogen synthase;  
 KW WSB1-1-D4 gene; ss.  
 XX Aegilops tauschii.  
 OS Key Location/Qualifiers  
 FH 1. 9287  
 CDS /\*tag= a  
 FT /note= "the start codon is not indicated; contains 146  
 internal stop codons"  
 XX WO9914314-A1.  
 PN 25-MAR-1999.  
 PD 11-SEP-1998; 98WO-AU000743.  
 XX 12-SEP-1997; 97AU-00009108.  
 PR 20-MAR-1998; 98AU-00002509.  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA (AUSU) UNIV AUSTRALIAN NAT.  
 PA (GOOD-) GOODMAN FIELDER LTD.  
 PA (LINA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
 PI Li Z, Morell M, Rahman S;  
 XX WPI: 1999-229525/19.  
 DR P-PSDB; AAY06919.  
 XX New isolated cereal plant enzyme genes used for, e.g. expression of  
 PT antisense sequences of granule bound synthase.  
 XX Claim 14; Page 103-115; 171pp; English.

CC The invention relates to a novel enzyme of starch biosynthetic pathway in  
 CC a cereal plant, where the enzyme is selected from starch branching enzyme  
 CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme  
 CC (DBE), with the proviso that the enzyme is not SBE I of rice, or SBE I of  
 CC rice or maize. The methods and products can be used for targeting  
 CC expression specifically to the endosperm of the seeds of cereal plants  
 CC such as wheat or barley. They can be used for the expression of e.g.  
 CC antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.  
 CC wt. glutenin, grain softness protein I, bacterial isomylase, bacterial  
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be  
 CC used for modifying the characteristics of starch produced by a plant. The  
 CC present sequence represents the wheat DBE genomic DNA sequence. (Updated  
 CC on 17-OCT-2003 to standardise OS field)

XX Sequence 9289 BP; 2477 A; 1909 C; 2040 G; 2863 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 3.71e-214 Length: 9289  
 Score: 2359.50 Matches: 655  
 Percent Similarity: 27.25% Conservativity: 7  
 Best Local Similarity: 26.97% Mismatches: 16  
 Query Match: 56.02% Indels: 1757  
 DB: 2 Gaps: 18

US-09-674-817b-3 (1-764) x AAX34655 (1-9289)

Qy 2 GlyProAlaProArgLeuArgArgTyrArgProAsnAlaThrAlaGlyLysGlyValGly 21  
 Db 1948 GGGCGGGCGCGCGCTCGGACGCTGGCGACCCGACCGCGCGGGGAGGGGCTCGG 2007  
 Qy 22 GluValCysAlaAlaValValGluAlaAlaThrLysValGluAspGlu---GlyGluGlu 40  
 Db 2008 GAGGTGTGGCGCGCGTGTTCGAGCGCGCGACGAAGCGCGGATGAGGACGACGAG 2067  
 Qy 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyCysArgValLeuAlaGly 60  
 Db 2068 GAGGAGCGGTGGCGGAGGACAGTACGCTCGCGCGCGCGTGCAGGGTGTCTCGCGGA 2127  
 Qy 61 MetProAlaProLeuGlyValAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80  
 Db 2128 ATGCCCGCGCGCTGGCGGCCACCGCTCGCGCGGGGTCAATTTTCGCGCTCTACTCC 2187  
 Qy 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97  
 Db 2188 GGTGGAGCCACCGCGCGCGCTCTGCTCTCTCAGCGCAGAGATCTCAAGGGCGGTGGG 2247  
 Qy 97 ----- 97  
 Db 2248 TTGCTCCCGTAGAGTTTCATCAGCTTTGCGTCCGCGCGCGCCCTTTCTGGCGTG 2307  
 Qy 98 -----Ala-AspArgValThrGluGluValProLe 107  
 Db 2308 CGATTTAAGTTTGTACTGGGGGAATGCTGCAGGATAGGCTGACGGAGAGGTTCCCT 2367  
 Qy 107 uAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGluLeuHI 127  
 Db 2368 TGACCCCTGTGAATCGAGCTGGAAACGTGTGGCATGTCTTATTGAAGCGCGAGCTGCA 2427  
 Qy 127 sAsnMetLeuTrpGlyTrpArgPheAspGlyThrPheAlaProHisCysGlyHisTrpLe 147  
 Db 2428 CGACATGCTTTACGGGTACAGTTTCGACGGCACCTTTGCTCCCTCAGCTCGCGGCACTACCT 2487  
 Qy 147 uAspValSerAsnValValAspProTyrAlaLys----- 159  
 Db 2488 TGATATTTCCAATGCTGTTGGTATCTTATGCTTAAGGTGATCATCTTTAGCTTTACCT 2547  
 Qy 159 ----- 159  
 Db 2548 GCATCTGGTATTTACAGTAAATTTGTAGTGGACCCCTATTGTTGGCTTTGTGTT 2607  
 Qy 160 -----AlaValIleSerArgGlyGlyTrpGlyValProAlaArgGlyAsnAsnCysTr 177  
 Db 2608 GCTCTAGCAGTGTAAAGCCGAGGAGTATGGGTTCCGGCGCGTGTGTAAACAATGTCG 2667

Qy 177 pProGlnMetAlaGlyMetIleProLeuProTyrSerThr----- 190  
 Db 2668 GCGTCAGATGGGTGGCATGATCCCTCTTCATATAGCAC-GGTATGCCCTGATTGCTGAAA 2726  
 Qy 190 ----- 190  
 Db 2727 ATATGGCTGCAATTGTTCTCTCTTTTCTCATATTTTCTTCCTGCTCTTCACCTGTGAC 2786  
 Qy 190 ----- 190  
 Db 2787 TACATTTGCCCTCAGACAGTCATGATCAAAGAGAGCAGTGTGTCATTAGACATTTTGTAGTTGTC 2846  
 Qy 190 ----- 190  
 Db 2847 TCGTGAATTTGACCAAACTTGTAAATTTACTGTTGTTAAAGTCTCTTGAATCATATTTT 2906  
 Qy 190 ----- 190  
 Db 2907 TTATAATATTATGTTTGGCAAGTGAAGTAAAGTGAATTCATCTAGTATTTTGTGTTGC 2966  
 Qy 191 -----PheAspTrpGI 194  
 Db 2967 TGTCTTAGTGTGTTAATTGGACATGCAGTAAAGGTTTTCATCTGCGAGTTTGTATGGGA 3026  
 Qy 194 uGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuAr 214  
 Db 3027 AGCGACCTACTCTTAAGATATCTTCAAAAGAGCCTGGTAATATATAGATGTCACCTTGGC 3086  
 Qy 214 gGlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVa 234  
 Db 3087 TGGATTCAGAAAGCATGATTCAGCAATGTAGAACATCCGGGTACTTTTCATTGGAGCTGT 3146  
 Qy 234 lSerLysLeuAspTyrLeuLys----- 241  
 Db 3147 GTCGAAGCTTGACTATTTGAAGGTACAGCTGTCTGTGCTACATAGGATAAATTTTA 3206  
 Qy 241 ----- 241  
 Db 3207 AAGAAAGCTACATATTAGCCAGAAATTTGGTTTATTACAAAACACTACTGCATACTAGCA 3266  
 Qy 241 ----- 241  
 Db 3267 GTTACATGCTCATTTATTCAGGAGAGATGCTCACACGCATCTTATTTGGATTTTATACCCAAT 3326  
 Qy 242 -----GluLeuGlyValAsnCysIleGluLeuM 251  
 Db 3327 TCTGTTTTCATATTGGACTGTTCCCTCTACAGAGCTTGGAGTTAATTGTTATGAATTAA 3386  
 Qy 251 etProCysHisGluPheAsnGluLeuGluTyrSerThrSerSer----- 265  
 Db 3387 TGCCCTGCCCATGATTCAGCTGAGTCAACGAGCTGGAGTACTCAACCTCTTCTTCCAAGTAAGGACATG 3446  
 Qy 265 ----- 265  
 Db 3447 AATTAGTATTAAGCTGCCGACGACTGTTTGGTGGAGAGTTTCATACACATTTTGTGCGCTGC 3506  
 Qy 265 ----- 265  
 Db 3507 ATAACCTGATATTGTTCAAACTATTATTTTATAGCAGTCACTCAACAGTTTTTACATATATA 3566  
 Qy 265 ----- 265  
 Db 3567 TATAATATAGACTATTTCGTCACCCCTGGGTGAGGAATAGTTATTCCTCCACCCTCTATT 3626  
 Qy 265 ----- 265  
 Db 3627 TTAAACATCTATGCACCGTAATTTTACGTTTCGTAATTTGCTCTTATTTTAGAGATAAAAA 3686  
 Qy 265 ----- 265  
 Db 3687 GAGAACGTAAGAAAAACCTATATATCGTCGTAAAAAATAATGTTACGTAAAAATTTACAAAT 3746

[illegible]

D5	4825	TATACATTTTACTCTCTAGAACTACTCTTTTTCATTTCTTTTCTGCTGCTGTGCTATTTTGATATG	4884
QY	377	-----	377
D5	4885	ATTAATTTGCAAGCTTGTGGGGTAAATCTTTTGGTCAGCATATGTATCTTTAAATGTC	4944
QY	377	-----	377
D5	4945	ACAAATACTAATGTCCTGGTGCTTATTGATTTGGCATCTTCAAATTCCTCCTCAATGAAA	5004
QY	378	-----	382
D5	5005	AGGGAAAACTACTGTATGTCCTCGTCAACTAATTTTACATTTTGTGTTCAGATACCTGGGT	5064
QY	382	lThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySe	402
D5	5065	GATGGAATGCATGTTGATGGTTTCGTTTGTATCTTCATCCATAATGACCAGAGGTTTC	5124
QY	402	I-----	402
D5	5125	CAGGTAATTTGTAATTTATTGTTTGTGCTGTGCTCTTTTCAGAAGATCTCTTAAAGAA	5184
QY	403	-----	418
D5	5185	TGTTCTTTTACAAAGTCGTGGGATCCAGTTAACGTGTATGGAGCTCCCAATAGAAGGTGA	5244
QY	418	pMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAs	438
D5	5245	CATGATCACAAACAGGGACACCTCTGTGTTACTCCACCACCTTATTGACATGATCAGCAATGA	5304
QY	438	pProIleLeuGlyGlyVallys-----	445
D5	5305	CCCAATCTTTGGAGGCGTCAAGTACTGTTTCATCCAACACCTGTGTGCTGTGTCGATT	5364
QY	445	-----	445
D5	5365	CAATTGTTTAAATATGTAATGATCAATTTCCCAATGTTGATAAGGAAAAAANAATGCAAG	5424
QY	445	-----	445
D5	5425	TAGCTCTCTTTATCTGCTTCTTGTGAGTTATGCTAAACATGTAGATACTACTATATTTCA	5484
QY	445	-----	445
D5	5485	ACTGTATATCTTGACATATATATGCTTCCTGGAGGCTCTCTTATTCCTTTCCCCCGT	5544
QY	446	-----	462
D5	5545	TGCAATTTATAGCTCATTTGCTGAAGCATGGGATGAGGAGGCCCTCTATCAAGTAGGTCAAT	5604
QY	462	heProHisTrpAsnValTrpSerGluTrpAsnGlyLys-----	474
D5	5605	TCCCTCACTGGAAATGTTGCTCTGAGTGGAAATGGGAA-GGTAAGGTACCTGTTTAAAGATT	5663
QY	474	-----	474
D5	5664	TGAATGGCAAATACTGTAGAAAATATAACTTATATTTGCGACATATATAGATAAAGCAA	5723
QY	474	-----	474
D5	5724	ATAATACGCAATCCACCTGAACTTTAAGGGGCACGCAGAAATTTATCCCGCATCTGTCTAC	5783
QY	474	-----	474
D5	5784	AAGAAATGATAACACATGTGCTGAATAGTGAAGTACTACTTCTCAAATGTCTGAATGAACG	5843
QY	474	-----	474
D5	5844	CACCTACTCTTGTGAGTGTCAACCGAGCAAGAANAATTTGAGTTTTTCTGCAAGAAATTTGT	5903
QY	474	-----	474

Db 5904 TCATGTTGTGTGTTATTATATCTCCCTCCGTCGGAATATTATTTGTCGAGAAATGGATGTA 5963  
QY 474 ----- 474  
Db 5964 TCTAGACGTATTTTGTAGTCTAGATACATCCATTTTATCCATTTCTGCAACAAGTAGTTC 6023  
QY 474 ----- 474  
Db 6024 CGGACGGGGAGTATCATTTAACAAATATATGATGTTTGAAGTAAATCCCCACGAATA 6083  
QY 474 ----- 474  
Db 6084 AGCATATAAGACGATATTGCTTTTGTGACTTGCAACACCTAAACCTCATTTGTTTCTCCTA 6143  
QY 474 ----- 474  
Db 6144 GGATTTGGGTGTCGAAGCAAGCAGCTGGTGATATTATTTACCTTTGCTTTTATTG 6203  
QY 474 ----- 474  
Db 6204 TAGCTTGATTTAGGGTGGCGAAAGGTTTGTAGCTTAGTAGTGTTTGTAAATATTATA 6263  
QY 474 ----- 474  
Db 6264 GTTTATGTATATCTCTCATTTGGGCACCTCCGTACTGGTCCCATAGAAAGATAAAATG 6323  
QY 474 ----- 474  
Db 6324 GAATGATGTCGGCCCAATAATTGTGACACACTGTTGCGCAITTTGATTTTATCAGGA 6383  
QY 474 ----- 474  
Db 6384 ATGGAAATTGAAATCGGTAAGAAACATTCGATATTAAAGCTTGATATATCTAATGCTGG 6443  
QY 474 ----- 474  
Db 6444 TGGATCTTTAAGAGGGAACATATGATCTCGTGTGCACTCCATCTTCAACTAAAAAATATG 6503  
QY 474 ----- 474  
Db 6504 TTGCACATCTCCACGTCACCTACTAGCTATTTTATCCAAAGTACTAACTTTGTGGTGT 6563  
QY 475 -----  
TyrAspIleValargGlnPheIleLysGlyThrAspGlyPheAlaGlyG 492  
Db 6564 CTCCTCAGTACCGGACATGTGCGCAATTCATTAAGGACGTGATTTGCTGGTG 6623  
QY 492 lyPheAlaGlyCysLeuCysGlySerProHisLeuTyr----- 504  
Db 6624 GTTTTGGCAATGCTTTGTGGAAGTCCACACCTATACCAGGTAAGTTGTGGCAATACTT 6683  
QY 504 ----- 504  
Db 6684 GGAAATGGGTTGAGTGAATGTCATCGATTTTATATATATACCATGATGATACACAT 6743  
QY 504 ----- 504  
Db 6744 GTAAATATAACGATATAGTGTATGATATGATTTGGCTAAGAAGTACTCCCTCCCT 6803  
QY 504 ----- 504  
Db 6804 TAGTAAAGTTAGTACAAAGTTGAGTCATCTATTTTGGAACGGAGGAGTATAAGTGTAT 6863  
QY 504 ----- 504  
Db 6864 AACTAGTGCATATATAGGTTTAAACCCCACTTGGCAATGGAAGAACATAGGGCTTT 6923  
QY 504 ----- 504  
Db 6924 CTAGTTATCTTATTTTGTGCTGTGAATAATCCACTGAAAAAATTCAGCCATGTCATT 6983  
QY 504 ----- 504  
Db 6984 TTTTAGGGGGGAGAGAACTATCATTTGATTTTCCCCCTTAAAAAAGCCATCTCAGATT 7043

QY 504 ----- 504  
Db 7044 TCATAGTAACCTTGCTTTTCTGTAAAGAAATGAANAACGACTTCATACATTTCTGTGCAATA 7103  
QY 504 ----- 504  
Db 7104 TAAGTGATACACTAGTGAATATATAGGTTTAAACACCAACTTGCCAATGAAGAAACA 7163  
QY 504 ----- 504  
Db 7164 TAGGGCTTTCTAGTTATCTTATTTATTTGCTGGTGAATAATCCACTGAAAAATCCAGCC 7223  
QY 504 ----- 504  
Db 7224 ATGTCAATTTTTPAGGGGGAGAGAACTATATATGATTTTCCCCCTTAAAAAAGCCATC 7283  
QY 504 ----- 504  
Db 7284 TCAGATTTCATAGGAACCTTGCTTTTCTGTAAAGAAATGAANAACGACTTCATACATTTCTGCG 7343  
QY 504 ----- 504  
Db 7344 GCGCTTACTTAGCTCGATGGATTTTGTAAAGATGAATGCCAAATTTATTTGGCGGATTTG 7403  
QY 504 ----- 504  
Db 7404 ATCGTTATTTCCAAATTTTCATTTTCTCTAGCAATCAACCCAGTACCTTTGTTATTGCG 7463  
QY 505 -----  
GlnAlaGlyGlyArgLysProTrpHisSerIleAsnP 517  
Db 7464 ACTGCAATTTCTTATGATTAATCAGGAGGAGGAGGAAACCTTGGCACAGTATCACT 7523  
QY 517 heValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrA 537  
Db 7524 TGGTATGTGCATGATGGATTTACACTGGGTGATTTGGT-ACATATAATATACCAAGTC-A 7581  
QY 537 snLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrAsnCysG 557  
Db 7582 ATTTACCAAAATGGGAGACCAATAGATGGAGAAATCACAATCTTAGCTGGAATTTG 7641  
QY 557 lyGlu----- 558  
Db 7642 GGGAGTAAATCTGAACCTCCTCTTTTGTGAAATTTTCATGCTTTACATAATAGTCAA 7701  
QY 558 ----- 558  
Db 7702 ATGGCTGACAAATGTGTTGTATGTTCTCTCTACCTAAACCGTTAAGGCAGTAAGATT 7761  
QY 558 ----- 558  
Db 7762 TCCCTACAAGATCTCTTTGTTGTTATGTTATTTTCTAGAGAAAAGTTGCTTCAATT 7821  
QY 558 ----- 558  
Db 7822 TTGTGCAACGCGGAGTACAGGAATTTGGTTTATAAATATTGATACAGGCTGACCATCGTT 7881  
QY 558 ----- 558  
Db 7882 ACTAATAGGGGAAACAATAAGCACATTTTTTTAATAGCAAGGCATCACCTTTGTTCCGT 7941  
QY 558 ----- 558  
Db 7942 TTCCAATGAATCACAGTATCCGAACCATTAAGTTTACAAAGTATGCGTAGAGAGAAATAA 8001  
QY 558 ----- 558  
Db 8002 AGTATCAACCGCGAGAAAACAGTTGTTTCAGGCGCAAGAGAGAAAAGGAACGATATGCTC 8061  
QY 558 ----- 558  
Db 8062 TATTACATCAACCTTTTAGCATTTAGGGACGACCAGCATCATCCCATCTTCAATCAACTG 8121

Qy	558	-----	558
Db	8122	GAGCGAGGTCACTCCAATCTTCTCAGCAGCCTCAGAGTGGTGAACCTCCCAAGCAAGTGC	8181
Qy	558	-----	558
Db	8182	ATCAGCATCCATCATCTGGGGGTTGGGCACATACCATGAGCACAAATCACCCTGAATTGTAT	8241
Qy	558	-----	558
Db	8242	GAATTTTCTCTGTATTACCTTTCAGCAGACACCCCTGCGGTATAAATGGTTTTAAATGACAG	8301
Qy	558	-----	558
Db	8302	CATGTTCTTCAGTTTGAGCAAAATTTGTGCAATTCGAAAGAAAGCTTTGAAATCATATGTGG	8361
Qy	559	-----	560
Db	8362	AACATGCACATTACATTTTCATCTGACATATAGGAAGGAGAGCCGACGTCGCATGCTCCT	8421
Qy	561	-----	577
Db	8422	CTAGACTCGAGGAATTCGCAAGATTGTCTGTCAAAGATTGAGGAAGAGCAGATGCGCA	8481
Qy	577	snPheValCysLeuMetValSerGln	586
Db	8482	ATTTCITTTGTTGTCTCATGTTTCTCAAGTAAGACTTATATCTGATCTCTTCAATTTTT	8541
Qy	586	-----	586
Db	8542	GAGATTGCCTGTTTTTTCACAAATGGCATATGTTGTGAGGTGAAACATCCAATCCCAGTATT	8601
Qy	586	-----	586
Db	8602	AATAGAGCCAAACATGAAGGAGTTGTTATCTGAGATATCTGCCAAAGTTGAAATCTTAGA	8661
Qy	586	-----	586
Db	8662	TTCACTTCTTCAGTATTTTCAGACCTTCTAAGCATTTTCATTTTTTTTTTCAATTGTTAG	8721
Qy	587	GlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrIysGlyIysAsnAsnAsn	606
Db	8722	GGAGTTCCAAATGTTTACATGCGCGATGAATATGGCCACACAAAGGGGCAACAACAAAT	8781
Qy	607	ThrTyrCysHisAspSerTyr	613
Db	8782	ACATACTGCCATGATCTTATGTTCAGTACAAATTTGGTCACATATGTTGTTCTAAGTAAC	8841
Qy	614	-----	619
Db	8842	TATCTTCAAATCTTTGCATTCATCCGTCATGGCTCTTCTGTAGTGTCAAATATTATTTTCGCTG	8901
Qy	619	pAspLysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArg	639
Db	8902	GGATATAAAGAACAATACTCTGACTTGCAGAAATCTCTGCTGCTCATGACCAAAATCCG	8961
Qy	639	glys	640
Db	8962	CAAGTAAGTATTCGGTTGAATAATTTCTGTGTAGAACCACTGAAGGTGCTCCCAACGCT	9021
Qy	640	-----	640
Db	9022	AACGGAGCAAGGTCAATTTCCACCCCTAATCAAGTTGGTGTCTTATTTGTGTATTTGA	9081
Qy	641	-----	655
Db	9082	TCTGCTGCACCTGAGGAGTGCAGGGTCTTGCCCTTGAGACTTTTCCAAAGCCCGAACG	9141
Qy	655	GluGlnTyrHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArgPheVal	675
Db	9142	GTGTCAGTGGCATGGTTCATCAGCCTGGGAAGCCCTGATTTGGTCTCGAAGTAGCCGATTCGT	9201
Qy	675	lAlaPheSerMet	679

Db	9202	TGCCTTTCCATG	9214
RESULT 12			
AAAD42891			
ID	AAAD42891	standard; DNA; 11779 BP.	
XX	AAAD42891;		
XX	XX		
DT	24-FEB-2003	(first entry)	
XX	XX		
DE	Maize sugary1 (SU1) gene.		
XX	XX		
KW	Maize; starch debranching enzyme; sugary1; industrial		
KW	starch processing industry; ds.		
XX	XX		
OS	Zea mays.		
XX	XX		
PH	Key	Location/Qualifiers	
FT	exon	1884..2333	
FT		/*tag= a	
FT		/number= 1	
FT	misc_signal	1920	
FT		/*tag= b	
FT		/note= "Transcription start site"	
FT	misc_signal	1922	
FT		/*tag= C	
FT		/note= "Transcription start site"	
FT	misc_signal	1971..1973	
FT		/*tag= d	
FT		/note= "Translation initiation codon"	
FT	intron	2334..2577	
FT		/*tag= e	
FT		/number= 1	
FT	exon	2578..2763	
FT		/*tag= f	
FT		/number= 2	
FT	intron	2764..2887	
FT		/*tag= g	
FT		/number= 2	
FT	exon	2888..2980	
FT		/*tag= h	
FT		/number= 3	
FT	intron	2981..3314	
FT		/*tag= i	
FT		/number= 3	
FT	exon	3315..3467	
FT		/*tag= j	
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FT		/*tag= k	
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FT	exon	3924..4000	
FT		/*tag= l	
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FT	intron	4001..4247	
FT		/*tag= m	
FT		/number= 5	
FT	exon	4248..4389	
FT		/*tag= n	
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FT	intron	4390..4480	
FT		/*tag= o	
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FT	intron	4589..4706	
FT		/*tag= q	
FT		/number= 7	
FT	exon	4707..4792	
FT		/*tag= r	
FT		/number= 8	



Db 2624 CGGAAACGTTGGCAGCTGTTCATCCAGGGGACAGCTGCACGGCATGCTCTACGGAT 2683  
Qy 133 YrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValV 153  
Db 2684 ACAGTTTCGATGGCGTGTTCGCCCTGAGCGGACAGTACTACGATGTGTCCACGTTG 2743  
Qy 153 alValAspProTyrAlaLys----- 159  
Db 2744 TGGTGGATCCATACGCTAAGGTGACGGCTGTTGTCTTTACTTTGGCTATGCGTGTGAGC 2803  
Qy 159 ----- 159  
Db 2804 TGTGACACATCAGAAACTGATTGCTGGGTGCTGTGCTCATGTTTATGTTGTTTACTTCT 2863  
Qy 160 -----AlaValIleSerArgGlyGluTyrGlyValProAla 171  
Db 2864 CTTGTTGTTGTTTCTCTAGCGAGCAGTGTGAAGCGAGGTGAATATGTTGTGCTGCG 2923  
Qy 172 ArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyrSer----- 189  
Db 2924 CCTGGTGTAGTTGTTGGCTCAAAATGGCTGGTATGATGCCCTCTTCCCTATAAAGTA 2983  
Qy 189 ----- 189  
Db 2984 AGCCAGAACTACTCTCGCTCACACTACTTCTCTGTTGTTTTCATGCTGTATCCTTCTCT 3043  
Qy 189 ----- 189  
Db 3044 TCCAGTTTATGATCTCCCATGCTGACTCACTCACGATTAACAATAAAGAAACCA 3103  
Qy 189 ----- 189  
Db 3104 CCGCATATATTGGCTCATTTGATGATTTGAAAGCTCCGCATGAACTAACTGAACAAG 3163  
Qy 189 ----- 189  
Db 3164 CGCTAGATCAACTGTAGTTAGGACTCATTTGGCTTCCTGTTACTTACTTCTGCTTT 3223  
Qy 189 ----- 189  
Db 3224 GCCAGTTCAAATGGAGTCGAAGTTATATTTCAGTCTATTCATGTTGTCTTTTATT 3283  
Qy 190 -----Thr-PheAspTrpGluGlyAspLeuProLeuAr 200  
Db 3284 CATTTGCTATGATAGGTTTTCGATTTGCAATTTGATTTGCAAGGTGACCTACCCCTGG 3343  
Qy 200 gTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAs 220  
Db 3344 GTACCATCAGAAGACCTTGTCTATATATGAATGCATTTTCGCTGGATTCACAAAGCACAA 3403  
Qy 220 pSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLe 240  
Db 3404 CTCAGCAGACAAACACCCAGGAACCTTACATTTGGTCTGTCTGTCTCAAGCTTACCATCT 3463  
Qy 240 uLys----- 241  
Db 3464 AAAGGTACTGTACGAACAGACTAGCTATAGTCTGCGAAAGTCTCTCATGCAATTTGTT 3523  
Qy 241 ----- 241  
Db 3524 TAGGTTTGGCACTATGCCAAGTAATGCTGCCCTAGTCTATTATAGTCAATAGGCATAACA 3583  
Qy 241 ----- 241  
Db 3584 CAGATTTTACTTTGTGCTTACATAAATGTTTTCCTCAGTAAACTTGTCTCAGTGGTATTGG 3643  
Qy 241 ----- 241  
Db 3644 TCGPCTTAGACTTTTGGCATGTGTTTGTGTTTGGAAATATAATATAGTGAATTTGTAAC 3703  
Qy 241 ----- 241  
Db 3704 CTTCTCCTATCAGCTTAAGCTTTTGGATAGAAAGAAATTGGTTGGTCACTGAATTAATA 3763

Qy 241 ----- 241  
Db 3764 TGGTATTAAAGACAGAGGTGCATGAATTCGAATCCTGACTAGCAACAATTAATAAACCCA 3823  
Qy 241 ----- 241  
Db 3824 AAAGCTTAAGCTTATAGGAGAGAGATGATATATTCCTTATATATATCTTAACATTTATG 3883  
Qy 242 -----GluLeuGlyValAsnCysI 248  
Db 3884 ACTAAACTCTTTGTTGTTGACCTGCATAACTCCCTTCACAGGAACCTTGGAGTGACTGAT 3943  
Qy 248 eLulLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerLys-- 267  
Db 3944 AGAGCTAATGCCCTGCCATGAGTTCAATGAGCTAGAGTACTTCAGTCTCTCTTCCGAAGTA 4003  
Qy 267 ----- 267  
Db 4004 TGTGGATTTGGATTACAGTATATAGATGCCATCATGTTTATAGGACTCTCGAACTGATAT 4063  
Qy 267 ----- 267  
Db 4064 CTTTTTGTTCATTGAGCATGATCGTATATGACCTTTTTCGTTCTATTTTCCATGATATTT 4123  
Qy 267 ----- 267  
Db 4124 CCCCCATTTCCAGATTTTCTAGTGTGATCTCCAAATTTTGTGCTTACCCCTTATAGCTTGA 4183  
Qy 267 ----- 267  
Db 4184 TCACAACTGACTTATATTCATATATTGACACATTAATTTTCATATAATTTGTTTCATCTTGTG 4243  
Qy 268 -----MetAsnPheTrpGlyTyrSerThrIleAsnPheSerProMetThrArgTyrT 286  
Db 4244 CCAGGATGAACCTTCTGGGATATTCACAAATAAATTTTCTCACCATGCAAGATATT 4303  
Qy 286 hrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValA 306  
Db 4304 CTTCAAGTGGCATAGAGACTCTGATGTGGTGCATTAATGAATTTAAAGCTTTTGTAA 4363  
Qy 306 rGluAlaHisLysArgGlyIleGlu----- 314  
Db 4364 GGGAGCCCAACAAAGGGGATTCAGGTAAACCAAGCAATTTAAAGTTAATGGCTGAATGC 4423  
Qy 315 -----Val 315  
Db 4424 TAACCGAAATAGAGCTTCTTATATATCATTTTTCACATGGAGATATGCTACTATTAGGTG 4483  
Qy 316 IleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSer 335  
Db 4484 ATCATGATGTTGTTCTTCAATCATACAGCTGAAGTAATGAGAAAGCCCAATATTATCC 4543  
Qy 336 PheLysGlyValAspAsnThrThrTyrMetLeuAlaProLys----- 350  
Db 4544 TTTAGGGGATAGATAAATAGTACTACTACATGCTTGCACCTAAGGTGAGATACATTATT 4603  
Qy 350 ----- 350  
Db 4604 CATCTTGTAAATCGTCTTTTCATGGACCACAAAGTATTTATGATTTCCATTCATAGATTC 4663  
Qy 351 -----GlyGluPheTyrAsnTyr 356  
Db 4664 ACGTCTATATAACAAGCTATTATTGAAGAGCATTTATTTGTGCAGGGAGAGTTTATAATTA 4723  
Qy 356 rSerGlyCysGlyValAsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAs 376  
Db 4724 TTTGGTTGTGGAAATACCTTCAATTTGAATCATCTCTGTAGTCCGTGATTTTATAGTGA 4783  
Qy 376 pCysLeu----- 378  
Db 4784 TTGCTTGGAGGTACAAATCTGTATATAAATCTGTATAAATTCCTTAATTTCTTCTGCCC 4843



QY 378 ----- 378  
Db 4844 GCTTGTCACTTAATGGATGATGCAAGTTTTTGAGGATGATAGCAATGTTATGCTTT 4903  
QY 378 ----- 378  
Db 4904 GCTGCTGAATATATAAGCAATTTAAATTTCTAGTATTCAAAACAAACAAAGAAACAAGT 4963  
QY 378 ----- 378  
Db 4964 TTTCTTTAATGATATTCGTCATTGACTATCAGTGTGTTAAGCTATATATTTGTTAAGAT 5023  
QY 379 -----  
Db 5024 AAATGTTTATGCACATAATTTGAGTTTGATGTTGCAGATCTAGGTTAACAAGAAATGCA 5083  
QY 386 sValaspGlyPheArgPheAspLeuAlaSerIleMetThrArgGly----- 401  
Db 5084 TGTGATGGTTTTGTTTTGACCTTGCATCTATATCTAGCTACCCAGAGGATGCAGGTAAATGT 5143  
QY 402 -----Se 402  
Db 5144 TATTCCTATTTCCTCTATTGTTGCTTTTAGGCAATCTTAAGCCAACTTTCTCTTAC 5203  
QY 402 rSerLeuTrpAspProValasnValTyrGlyAlaProIleGlyAspMetIleThrTh 422  
Db 5204 CAGTCTATGGGATCCAGTTAATGTTGATGTAAGTCCAATGGAAGGTGACATGATTACGAC 5263  
QY 422 rGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuG 442  
Db 5264 AGGACACCTCTGTTGCCCCACCACCTATTGATGATGATGATGATGATGATGATGATGATG 5323  
QY 442 yGlyVallys----- 445  
Db 5324 AAATGTCGAAGGTAGCTGTATATTTTATCTATTGTTTATTTTCTCCAAAGCGC 5383  
QY 445 ----- 445  
Db 5384 AGGAACTGCGCCCGTTATATATTAAGAAAGAGAAACAAAGGTCTATAGAACCCA 5443  
QY 445 ----- 445  
Db 5444 GATAAAGACTCTCTTACGGAGGCCAGAAACAGCATACAAAAAAGTGTCCATAAGAC 5503  
QY 445 ----- 445  
Db 5504 ACTAACCTCCAAACATCTGCCCTTAAGCATTAGGAAGCGAGCCAACTACATTCGGGGC 5563  
QY 445 ----- 445  
Db 5564 CCTAGCCAGGTCTAGTGAGCCTAGATTTTGTAGCTCCAGCCATACCCCAACATACAGTTC 5623  
QY 445 ----- 445  
Db 5624 ATCTAAGAAGCTTCTCTGTAGTCTTGTAGTGAAGGAGATTCCACATTGAAGATTACTTT 5683  
QY 445 ----- 445  
Db 5684 GTTGGGTGAAGCCATACACACCACGCCGCCCCAGAAATGATGACACTGTTGAGCCCCCTTT 5743  
QY 445 ----- 445  
Db 5744 TCCTACTTTTGTGCCCTTAATAACAGAGCTCTCCACCCTCCGCGAAGAGGTTTCATC 5803  
QY 445 ----- 445  
Db 5804 AACAGCAGGATAAGGTGGCCAGCTGAAGAGGAGATAAAATACTGAACCAAAATTGACG 5863  
QY 445 ----- 445  
Db 5864 GGTAAAGATGCATGAGGTAGGAGGTACTGAATTGTTTCCAGTTGTTGATCATCAATAGGA 5923  
QY 445 ----- 445

Db 5924 GCAAGCATCTGGATGTGGGMAAACCTCTCTTTCTAAACCTGTGACGCGTCCAAACACTATT 5983  
QY 445 ----- 445  
Db 5984 CCTCATAGCAACACACAGGAAGAATTTGCATTTTCGGAGGAGCCCATGTCTTCCAAAGCCT 6043  
QY 445 ----- 445  
Db 6044 TTTCCATGGCTCAAAGGTGGTTGAACCTGAGATAAGATTTTTCACAAAGATTTAGACGA 6103  
QY 445 ----- 445  
Db 6104 GAAATTCCTGAGATCTCATCTCCACCTGTCTGATCAGGAACCTTGGGATAATTCAAC 6163  
QY 445 ----- 445  
Db 6164 CCCTCACTGAATCCOATAACAGCAGGTACTGTGCAGCCAGCCAGCAGAGAGGTGCT 6223  
QY 445 ----- 445  
Db 6224 TTAATATCCCTAACCCACTGCCAATTTTCAAGGGCTCGAGCCACAGTTCTTGAATATAGA 6283  
QY 445 ----- 445  
Db 6284 AATCTTTTGGCCACCTTAGCTACCACTCAGGGGCAAAATCCCTGATCGAGCCCATTT 6343  
QY 445 ----- 445  
Db 6344 AGCCATCTATCAGTCCAGAAAAGAGTGTGGTGCCATTCCTCAACCATAGAAATCGAGAA 6403  
QY 445 ----- 445  
Db 6404 TCTGAAAACAGATTCTTGACATGCTGCTGTATAGGAGCTTCAGTCCCTGCCAGGCCTG 6463  
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QY 445 ----- 445  
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QY 445 ----- 445  
Db 6584 ACCAGACAGCTGCTCCATTAGCCTCTTCTCTCTTCTTCCAAATAAAACCCCTTCTAAT 6643  
QY 445 ----- 445  
Db 6644 TTGCTATAGCTTTAATCATCCAAATTGGATATTCATTCGAATAAGAGATAGACTGGAT 6703  
QY 445 ----- 445  
Db 6704 AGCCGAAGSCACATATCGCACAGAGCTATTCTACCAGCAAGGTTAAGAAGATGTGCTTT 6763  
QY 445 ----- 445  
Db 6764 CCAATTTGCAATAAGAAGTTATTGTTGTTGATTATGATTCTTAATCTTATTTTATCA 6823  
QY 445 ----- 445  
Db 6824 TCTGCACCTAACTGAAGATTCAAGCCATTTTGTGGTTTGGTATACGTGTACACATGCTAT 6883  
QY 445 ----- 445  
Db 6884 GTAACCTAATCTCAGTTACCATGTGCTGTGATGCTTTTGGTAAATATATGAACCTGATGCG 6943  
QY 445 ----- 445  
Db 6944 TGTAAATATGCGAAGCAGTATATATAATAATTCGACTGTATCAACATATTGATTGTTCTT 7003  
QY 446 -----  
LeuIleAlaGluAlaTrpAspA 453  
|||||

D5	7004	GGTTTTGTTCTCACTCTCTCCATGTATATATAGCTCAATTGCTGAAGCATGGGATG	7063	QY	503	-----	503
QY	453	laGlyGlyLeuTyrglnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnG	473	D5	8143	AAAGTCCATTCTATGTAGTAGTAGTATAA	8202
D5	7064	CAGGAGTCTCTATCAAGTTGGTTCAGTTCTCTCACTGGAACGTTTGGTCAAGTGAATG	7123	QY	503	-----	503
QY	473	lyLys-----	474	D5	8203	TCCTTTCTTTCAGTGTCTAATGAGACCTCTTCAAGCCATTGAAACTCTCTACTATATATGT	8262
D5	7124	GAAAGGTAAGATACTTTCAAGAGACTTCAAAAGTCTTTTGTCTACTTGGTACTTTCTAAATA	7183	QY	503	-----	503
QY	474	-----	474	D5	8263	ATTTTGTGGATGAGAGACCGCATCAATAAATATCTCTCTGTGAAGTGAAGCAT	8322
D5	7184	ACAAATGAAGCCTTGTCAAAATACAGAATGTAAGTTTCAACAGATATATTAAATAGATGA	7243	QY	503	-----	503
QY	474	-----	474	D5	8323	TAACAATGAATGCGGAATACTCTCAATGTATTGTATGTCAATTAGGTGGATTAGTGTATC	8382
D5	7244	GTGCTTCTATCTACCTGTGAATTTGTCAGGGATCTAAACTGTTTAAATTTCTAATGTT	7303	QY	504	-----	510
QY	474	-----	474	D5	8383	TACAAATAATAGTTGGTATTGATTAAGTACATGCTTTTATTATCAGCGAGGGGGAGGA	8442
D5	7304	AGTTTCTCTAGAGGCAAAATCGTAATTTGGTCTGTGTAAGTGGATACAGTTTGGATAAT	7363	QY	510	ysProTrpHiserileAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuV	530
QY	474	-----	474	D5	8443	AGCCTTGGCAGATATCACTTTGTATGTGCACAGATGGATTACACTGGCTGATTGG	8502
D5	7364	GGATGAACCAAGATCTACGTTTCAAGGCCCACTATCAACAGACTCAGGGCTGTTGGGG	7423	QY	530	alThrTyAsnLysLysTyAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnH	550
QY	474	-----	474	D5	8503	TCACATACAAATAGCAAGTACAACTTGTCAAATGGTGGAGCAACACAGAGATGGGAAATC	8562
D5	7424	GCAAGTCCAGTTCAGTTTCAAGCTTCTGAAGAGCTGGCTCCAAGAACCTGAGCCT	7483	QY	550	isAsnLeuSerTrpAsnCysGlyGlu-----	558
QY	474	-----	474	D5	8563	ATAATCTTACGTGGAATTTGTGGGAGGTAATTTGAAATCTCATGCTTTTATCTCTCTAG	8622
D5	7484	AGGATCTTGGATCTCATATTATGTTTGTGTTCTAGAGAAGCTGGTTTCAAGAGGCC	7543	QY	558	-----	558
QY	474	-----	474	D5	8623	GCTTTTATGTAGTCAAAATGCTGTCAAATGCATCTGTATAGTATTTCTAGCCATGAGTA	8682
D5	7544	AACACTTAGGACTTCCCAGCCCAACTGTTTATGTGTTGAGCAGAGAAGCCAGCTA	7603	QY	558	-----	558
QY	474	-----	474	D5	8683	CCAAACTGGTTTCACTAAACAGGCTATATAGTTTGTACAGTGCATTTCCAGCTAAATT	8742
D5	7604	GACAGAAACACAAATACACTGCAITTTGTTGGACTTATAGATTTTAAATTTATAACACA	7663	QY	558	-----	558
QY	474	-----	474	D5	8743	TATGTGGCAAGTATATACAGATCATCTCTATAGTGTAGCGACCTTTAGAGTTTCATTGA	8802
D5	7664	AGAATGATTTTGGATATACTTTCACAGGCCAACACTTAGGAGTATGTTTCAACAATAG	7723	QY	559	-----	575
QY	474	-----	474	D5	8803	ATAATCGAGGAAGGAGAAATTTGCAAGTCTGTCAAGTCCGAAGATTAAAGGAAGGCAATG	8862
D5	7724	CCTCACTGACAAACATTAGGTAAAGTGCATCTTTGATCTTTATCAGAGCATGATGCTGATGA	7783	QY	576	AsAsnPhePheValCysLeuMetValSerGln-----	586
QY	474	-----	474	D5	8863	CGCAATCTTTTGTGTTGTTCTATAGTTTCTCAGGTAAGNATTAGTATCTGTGTTTTTAAG	8922
D5	7784	AGTTTGTGTAATTAACCATATGATCTTTTGCATCTCTTTCAGTAAACCAACAGCTTCCA	7843	QY	586	-----	586
QY	475	-----	475	D5	8923	TTTTTATGGAATGTGCTTTCAAGTCCCTGTTTGTTCAGGGTAGAACTCAAGGTTGCATT	8982
D5	7844	ACTTTTGTCTCTATAGTTGTTTCCAAAGTACTAACTTGTCTAGTTGTTTCTCAGT	7903	QY	586	-----	586
QY	475	yrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaG	495	D5	8983	TGCAGTCAGTGGTATGCTGGAATATGATCATCTGTTTCACTCTTGTAGTTAGTCACTTG	9042
D5	7904	ATCGCGATACCGTGGTTCAGTTTCATCAAAAGGCACAGATGGATTGCTGGTCTTTTGTCTG	7963	QY	586	-----	586
QY	495	luCysLeuCySglySerProHisLeu-----	503	D5	9043	ATGAGGGTTTACTTGTCTAAGTGTGTGTGAGGATCTGTGTTTTTCCAAAAGATTATGCCA	9102
D5	7964	AATGCTTATGTGGAAGTCCACA-GTTATACCAGGTAATGTAGCATAGTACCCATCAATG	8022	QY	586	-----	586
QY	503	-----	503	D5	9103	TGTTGCATTAATATCCAACTAGTGTATTTGTACTCTGAGAAACATATTTATTATTAAACA	9162
D5	8023	AGCACGGTGTACATGACCTGAACAGAAACTTTTGAAGGAACCTTTTGAAGGAAGTGTACAG	8082	QY	586	-----	586
QY	503	-----	503	D5	9163	AAAATTACTGTAAACATCATTTATTGTGCAAGGTTTCAGTCTTCCATGTCATCTAATAT	9222
D5	8083	ATAAACAGAAATPAACATAATATGACAATCTAGCATATATTTTCAAGCTTAGAAGTTTAAAC	8142				

QY 586 ----- 586  
Db 9223 AGGGTAAGTTAAAGTGGATCTCGAAGTCACATTGTTATTTTTTGTATGATCTACTACT 9282  
QY 587 ----- GlyValProMetPheTyrMetGlyAs 595  
Db 9283 ACCTATCAATGTTTTCATTCTTAAATTTTTAGGGAGTTCCAAATGTTCTACATGGCGGA 9342  
QY 595 pGluTyrClyHisThrIysGlyGlyAsnAsnThrTyrCysHisAspSerTyrVal-- 614  
Db 9343 TGAATATGTCACACAAAGGAGGAGGAACAACAAATACGTACTGTCATGACCATTAATGT-CA 9401  
QY 614 ----- 614  
Db 9402 GTCCGATGCCAACACATATTAAACATTTGTTTAAATCAATTTCTTTGACATTTCTGTAAT 9461  
QY 615 ----- AsnTyrPheArgTyrAspIysLys---G1 623  
Db 9462 CTTCTAGCCTTTTATTTTGGTGTGCAGGTCAACTATTTCGTTGGGATGAAGAAGA 9521  
QY 623 uGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrIysPheArgLys----- 640  
Db 9522 ACAATCCTCTGATTTGTACAGATTCTGCCGTCTCATGACCAAAATTCGCAAGTAATACTC 9581  
QY 640 ----- 640  
Db 9582 TTCCCGCCAAATATTTCGTCGTATACCGATGATGTTTCATCTCTTCAACCAATGGCGAG 9641  
QY 641 -----G 641  
Db 9642 ATCTGTACAGTTTACGTTGTCTACTGTCTATTCATGTTCTTTTGGTGTGCAATACAGGG 9701  
QY 641 luCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTyrPheIsglyH 661  
Db 9702 AATGTGAATCTCTTGGCTTGAGGACTTCGAGCTTCAGAACGGTTGAATGSCACGGTC 9761  
QY 661 isGlnProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPheSerMet---- 679  
Db 9762 ATCAGCCGGGAGCCCTGACTGTGTCAGAGGCAAGCCGATTCGTTGCCTTCACCATGTAC 9821  
QY 679 ----- 679  
Db 9822 TGACATAACACCTACCACCATCATCACTAGTCATTTCAAGATCATTTTCTACCATTA 9881  
QY 680 -----LysA 681  
Db 9882 GTAATCAGAAGATCAAAAAGAGAGTGTGATGTTTCTATGTATCTGTTACTGCAGAGG 9941  
QY 681 spGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValG 701  
Db 9942 ACGAACCAGGCGGAGATCTACGTGGCTTCACACCACTGTCACCTTCGCGTGTGTCG 10001  
QY 701 luLeuProGluArgAlaGlyArgTyrGluProValValAspThrGlyLysProAlaP 721  
Db 10002 GGCTTCAGAGCGCTCTGGTTCGATGGGAGCGGTGGTGAGACCGGCAAGAGGCAC 10061  
QY 721 roTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerH 741  
Db 10062 CATATGACTTCTCACCAGATGGCTACCATGCTGTGTGTACCGCTGTACCATCTCTCTC 10121  
QY 741 isPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuA 761  
Db 10122 ATTTCCTCAACTCCAATCTCTATCCCTATGCTCAGTACTCTCTCATCTATCTTGTATTC 10181  
QY 761 rgProAspVal 764  
Db 10182 GCCCTGATGTC 10192  
RESULT 13  
AADA47817  
ID AAD47817 standard; DNA; 10439 BP.  
XX  
AC AAD47817;

XX 24-FEB-2003 (first entry)  
XX Alternative version of maize sugary1 (SU1) gene.  
XX Maize; starch debranching enzyme; sugary1; industrial application; SU1;  
XX starch processing industry; ds.  
XX Zea mays.  
XX US6410716-B1.  
XX 25-JUN-2002.  
XX 24-FEB-1999; 99US-00256741.  
XX 24-MAR-1995; 95US-00410784.  
XX (IOWA) UNIV IOWA STATE RES FOUND INC.  
XX Myers AM, James MG;  
XX WPI; 2002-616514/66.  
XX Novel starch debranching enzyme protein sugary1 or its polypeptide  
XX fragment useful as replacement for bacterial and fungal enzymes currently  
XX used in starch processing industry.  
XX Disclosure; Fig 2; 75pp; English.  
XX The invention relates to maize starch debranching enzyme, sugary1 (SU1)  
XX and nucleic acid molecules encoding such proteins. SU1 sequences are used  
XX as a replacement for the bacterial and fungal enzymes currently used in  
XX the starch processing industry and as immunogens to raise antibodies  
XX against SU1. Polynucleotides of the invention are useful as markers for  
XX identification of specific corn varieties, for the development of corn  
XX varieties with starch properties tailored for specific industrial  
XX applications. The present sequence is an alternative version of maize SU1  
XX gene. Note: This sequence is stated to be the same as that shown as SEQ  
XX ID NO:3 (AAD42891) in column 41-52 of the specification. However the  
XX sequences differ  
SQ Sequence 10439 BP; 2847 A; 2237 C; 2187 G; 3168 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7,81e-197 Length: 10439  
Score: 2179.00 Matches: 649  
Percent Similarity: 25.80% Conservative: 46  
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Query Match: 51.73% Indels: 1937  
DB: Gaps: 21

US-09-674-817B-3 (1-764) x AAD47817 (1-10439)  
QY 2 GlyProAlaProArgLeuArg-ArgTyrProAsnAlaThrAlaGlyLysGlyValG1 21  
Db 801 GGGCGCGTGGCGCGCGCGCGTGGCGCGCGCCCAAT---GTGGCGGACTGGCGCGGGG 857  
QY 21 yGluVal-----CysAlaAlaValValGluAlaAlaThrLysValG1 35  
Db 858 GCGGCTGTCTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGA 917  
QY 35 uAspGluGlyGluGluAspGluProValAlaGluAspArgTyrAlaLeuGlyGlyAlaCY 55  
Db 918 GGACGACGACGACGACGACGAGGAGTGGCGGAGGAGAGTTCGGCTGGCGCGCGCGTG 977  
QY 55 sArgValLeuAlaGlyMetProAlaProLeuGlyValAlaThrAlaLeuAlaValAs 75  
Db 978 CCGGCTGTTCGGGAATGCCCGCGCGCGCTCGGGCCACCGCGCTCCCGCGGTGTCAA 1037  
QY 75 nPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAs 95  
Db 1038 CTTCCCGCTACTCCAGCGGTGCTCGCGCGCGTGTGCTGTGCTCTTCGCTCCCGCGGA 1097







```
Db 7634 GGTTCATTTCAGTCAGTGTATGCTGATATGATCATGTTGTTGAGTCTTGTAGTTT 7693
QY 586 -----
Db 7694 AGTCACCTTGATGAGGGTTACTACTTGTCTAAGTTGTTGAGGATCTGTGTTTCCAAAG 7753
QY 586 -----
Db 7754 ATTATGCCATGTTGCATTGATATCCAACTAGCTGTATTTGTACCTGAAGAAACATATTT 7813
QY 586 -----
Db 7814 ATTTAAACAAAAATTACTGTAAACATCATTTATTGACAAAGTTTCAGTCTTTCCATGCA 7873
QY 586 -----
Db 7874 TCCTAATATAGGGTAAGTTAAAGTGAATCTGAAGTCACATGTTATTTTTGTATTGA 7933
QY 587 -----
Db 7934 TCTACTACTACCTATCAATTGTTTTCATTCTTAAATTTTAGGAGATTCATGTTCTA 7993
QY 592 xMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspse 612
Db 7994 CATGGCGCATATATGTCACAAAGGAGGAGAACACAAATACGTACTGCCATGACCA 8053
QY 612 rTyrVal-----
Db 8054 TTAATGT-CAGTCCGATCCACACATATTAAACATGTTTAAATCAATTCCTTGACAT 8112
QY 615 -----
Db 8113 TCTTGAATCTTCTAGCCTTTTATTTTGGTGTGCGAGTCAACTATTCGGTTGGATAA 8172
QY 621 sLys---GluGlnTyrSerGluLeuHisArgPheCysLeuMetThrLysPheArgly 640
Db 8173 GAAGGAAGAACATCTCTGATTTGTACAGATCTGCCGTCTCATGACCAATTCGCGAA 8232
QY 640 s-----
Db 8233 GTAATACTCTCCCGCCAAATATTTCGTCGTATACCGATGATGGTTTCATCTGTTCCACA 8292
QY 640 -----
Db 8293 AATGGCGAGATCTGTACAGTTTACGTTGTCATCTCTATTTCATGTTCTTTTGGTGTC 8352
QY 641 -----
Db 8353 AATACAGGGATGTGAATCTCTTGGCTTGAGGACTTCCGACTTCGAGAACGGTTGAAT 8412
QY 658 rPheHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheS 678
Db 8413 GGCACGGTCATCAGCCCGGAGCCTGACTGTGTGTCAGAGCAAGCCGATTCGTGTCCTTCA 8472
QY 678 erMet-----
Db 8473 CCATGGTACTGCATTAACACCTACCACCATCATCTACTGATCTTCAAGATCATTTTC 8532
QY 679 -----
Db 8533 TACCATTAACTAATCAGAGATCAAAAAGGAGTGTGATGTTTCTATGATCTGTATC 8592
QY 680 -----
Db 8593 TGCAGAGGACGAAACCAAGGGGAGATCTAGTGGCCTTCAACACCACTACCTCCCG 8652
QY 698 laValValGluLeuProGluArgAlaGlyArgTrpGluProValValAspThrGlyL 718
Db 8653 TGGTTGTGGGCTTCCAGAGCGCTCTGGGTTCCGATGGAGCGGTTGGTGGACACGGCA 8712
QY 718 ysProAlaProTyrAspPheLeuThrAspLeuProAspArgAlaLeuThrIleHisG 738
```

```
Db 8713 AGGAGGCCACCATATGACTTCTCCTACCGATGGCTACAGATCGTGTGTCACCGTCTACC 8772
QY 738 lnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleL 758
Db 8773 AGTTCTCTCATTTTCTCTCAACTCCAATCTCTATCTATGCTAGCTACTCTCTCCATCATCC 8832
QY 758 euValLeuArgProAspVal 764
Db 8833 TTGTATTGGCCCTGATGTC 8852
RESULT 14
AA333162
ID AAX333162 standard; DNA; 1663 BP.
AC AAX333162;
XX
XX
06-JUL-1999 (first entry)
DE Potato isoamylase type DBE genomic clone SEQ ID NO:14.
XX
XX Potato; isoamylase debranching enzyme; DBE; starch; ss.
XX
XX Solanum tuberosum.
XX
XX WO9912950-A2.
XX
XX 18-MAR-1999.
XX
XX 04-SEP-1998; 98WO-GB002665.
XX
XX 06-SEP-1997; 97GB-00018863.
XX
XX (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Jobling SA, Schwall GP, Westcott RJ;
XX
XX WPI; 1999-229220/19.
XX
XX P-PSDB; AAY04382.
XX
XX New isolated potato isoamylase-type debranching enzyme gene.
XX
XX Claim 7; Fig 8; 72pp; English.
XX
XX The present invention describes a novel nucleic acid sequence which is
CC obtainable from potato plants and carries at least a portion of an
CC isoamylase-type debranching enzyme (DBE) gene. Constructs containing the
CC nucleic acid sequence can be used to alter the starch properties of
CC plants such as potato, sweet potato, maize, wheat, barley, oat, cassava,
CC pea or rice. The starch can have increased branching and/or shorter chain
CC length, reduced peak viscosity, higher setback viscosity or increased
CC viscosity onset temperature. By using an antisense sequence with greater
CC homology to the native gene, greater inhibition can be achieved
XX
XX SQ Sequence 1663 BP; 503 A; 312 C; 381 G; 467 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 8,71e-170 Length: 1663
Score: 1884.00 Matches: 333
Percent Similarity: 86.30% Conservative: 45
Best Local Similarity: 76.03% Mismatches: 58
Query Match: 44.73% Indels: 2
DB: 2
US-09-674-817B-3 (1-764) x AAX333162 (1-1663)
```

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QY 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343
Db 39 ACGCCCAAGTGNATTCGAGCTCGGTACCCGGGGATCCGATTCAGGCATTTGACACAGGTGTG 98
QY 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
Db 99 TTTTATACGCTAGCTCCTAAGGGTGAATTTTACAATCTACTCAGGATGTGGAAATACCTTC 158
```



364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTrpValThr 383  
159 AACTGTAATAATCCCAATGCTACGTCATTAATAGTGGATTTGGTGGATTTACC 218  
384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403  
219 GAATGCGATAGATGGCTTCCGCTTGTATCTTCTATCTTACACAGAGTACGAGC 278  
404 LeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrGly 423  
279 TCGTGAATGCTGTAATGCTATGAAATTCATATTCAGCGTACGATCATCACAGGC 338  
424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGly 443  
339 ACTCCTCTCACAGCCCAACCATTTGATGATGATGATGATGATGATGATGATGATG 398  
444 ValIysLeuIleAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463  
399 GTAAAGCTTATAGTGAAGCATGGATTTGTGGAGGCTTTACCAAGTTGGCATGTTCCG 458  
464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483  
459 CACTGGGCTATCTGGTCGGAGTGGAAAC--GAAGTACGTACATGTCGGAGTTTCATC 515  
484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503  
516 CAAGGCACTGATGGTCTTCTGGGCTTTGCTGAATGCTTTGTGGAAGCCCAATCTTA 575  
504 TyrGlnAlaGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGly 523  
576 TACCAGAAAGGAGGAGAAACCATGACAGCATGATTAATTTCTGTCGCCACGATGTT 635  
524 PheThrLeuAlaLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsn 543  
636 TTACTTTGGCTGATTTAGTGACATACACAAATAAACACATTTGGCAATGGAGAGGAC 595  
544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyPheAla 563  
696 AACAAAGCGGGAGATCAATCAATATAGTTGGATTTGTGGAGGAGGAGAAATTTGCA 755  
564 ArgLeuSerValIysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMet 583  
756 ACTATCTTTATGAAGAATTTAGGAAAGAAACAAATGGGAACCTTCTCTGCCCTTATG 815  
584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603  
816 GTTTCCCAAGGTGTTCCCATGATATATGGGGATGATATGGTACACATAAGGAGGAGGA 875  
604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLys--- 622  
876 AACAAACACAGTATGCCATGATTAATATATTAATTTCTGCTGGGATAGAAGGAT 935  
623 GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGlyCys 642  
936 GAATCTTCATCTGATTTTTCAGATTTTGGGCTCATGACCAAAATTCGCCCATGAATGT 995  
643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662  
996 GAATCACTGGATTTAGATGGTTTCCCTACAGCAAGGAGGCTGCAATGGCATGTGCACACT 1055  
663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682  
1056 CCTAGAACTCAGATTTGCTGAAACAAAGTCGATCTGTCATTCACACTGGTCGACAAA 1115  
683 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702  
1116 GTGAAGGAGAGCAATATATATGCTTTAAACCCAGCCCATTTGCTGTGAACGATTTACACT 1175  
703 ProGluArgAlaGlyArgArgTrpGluProValValAspThrGlyLysProAlaProTyr 722  
1176 CCAGATAGGCTGGTTATAGATGGCCGCTTTGTGGACACAGGCAACCAACGACCACTTT 1235  
723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742

1236 GACTTCTTGACAGACGAGTCTCTGAGAGAGACAGACAGCAGCAACAATATCTCATTTT 1295  
743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeu 760  
1296 CTGACGCGAACCATGATTCGATCTCAGTTATTCATCCATTTATCTTTACTA 1349  
RESULT 15  
AAAX27062  
ID AAAX27062 standard; DNA; 2634 BP.  
XX  
AC AAAX27062;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE S. tuberosum isoamylase clone 9 coding sequence.  
XX  
KW Isoamylase clone; potato; branched polysaccharide synthesis; amylopectin;  
KW starch modification; debranching activity; ss.  
XX  
OS Solanum tuberosum.  
XX  
PN WO9906575-A1.  
PD 11-FEB-1999.  
XX  
PF 30-JUL-1998; 98WO-GB002280.  
XX  
PR 31-JUL-1997; 97GB-00016185.  
XX  
PA (PLAN-) PLANT BIOSCIENCE LTD.  
XX  
PI Edwards EA, Smith AM, Martin CR, Bustos Guillen R;  
XX  
DR WPI: 1999-153803/13.  
DR P-PSDB; AAY00870.  
XX  
PT New nucleic acid from potato encoding starch debranching enzyme with  
PT isoamylase activity - and related vectors, transformed cells and plants,  
PT proteins and antibodies, used to generate starch with altered properties,  
PT for use in foods, as thickeners etc.  
XX  
PS Claim 3; Fig 3; 78pp; English.  
XX  
CC This sequence encodes a Solanum tuberosum isoamylase of the invention.  
CC Fragments of the isoamylase coding sequence are used to identify and  
CC clone isoamylases from other plant species, by standard hybridisation or  
CC amplification methods. Expression of the isoamylase DNA in host cells is  
CC used to produce the isoamylase which is used: (i) to raise antibodies  
CC (Ab) (for identification, isolation and localisation of isoamylases); and  
CC (ii) for synthesis of branched polysaccharides. The DNA, proteins and Ab  
CC (or related peptides) are used to alter the quality and quantity of  
CC polysaccharides in a host cells, specifically to alter branching in  
CC amylopectin. The modified starches produced are useful in human or animal  
CC foods; as biodegradable plastic; as food or paint thickener; in starch-  
CC coated films, paper and textiles; in mining explosives; in  
CC pharmaceuticals and glues. Manipulation of debranching activity in a  
CC plant allows control of starch properties, e.g. increased gel strength;  
CC formation of paste rather than gel, changed physical characteristics etc  
XX  
SQ Sequence 2634 BP; 854 A; 496 C; 573 G; 711 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 3,698-140 Length: 2634  
Score: 1577.00 Matches: 329  
Percent Similarity: 59.9% Conservative: 111  
Best Local Similarity: 44.04% Mismatches: 235  
Query Match: 37.44% Indels: 72  
DB: 2 Gaps: 19  
US-09-674-817B-3 (1-764) x AAAX27062 (1-2634)  
QY 30 AlaAlaThrLysValGluAspGluClyGluGluAspGluProValAlaGluAspArgTyr 49

[illegible]

Tue Aug 10 12:22:09 2004

us-09-674-817b-3.p2n.rng

Page 32

Qy 752 SerTyreSerValIleLeu 758  
Db 2297 COGTACTGCTATGCTTCTT 2317

Search completed: August 10, 2004, 01:34:49  
Job time : 842 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 10, 2004, 00:58:30 ; Search time 135 Seconds  
(without alignments)

3140.611 Million cell updates/sec

Title: US-09-674-817B-3

Perfect score: 4212

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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3569.5	84.7	2700	4	US-09-731-166-15
2	3528.5	83.8	2712	2	US-08-410-784A-1
3	3029	71.9	2706	4	US-09-463-238-2
4	2923	69.4	2806	4	US-09-463-238-11
5	2612	62.0	2133	3	US-09-187-124-1
6	2612	62.0	2133	4	US-09-850-936-1
7	1577	37.4	2634	4	US-09-463-238-3
8	1305.5	31.0	1230025	4	US-09-198-452A-1
9	1225	29.1	4403765	3	US-09-103-840A-2
10	1225	29.1	4411529	3	US-09-103-840A-1
11	1187	28.2	2181	3	US-09-129-075-3
12	1187	28.2	2181	3	US-09-346-237-12

13	1187	28.2	2181	4	US-09-544-123-3	Sequence 3, Appli
14	1122.5	26.7	1944	4	US-09-252-931A-8062	Sequence 8062, Ap
15	1032.5	24.5	1389	4	US-09-463-238-12	Sequence 12, Appli
16	1014	24.1	1830121	4	US-09-557-884-1	Sequence 1, Appli
17	1014	24.1	1830121	4	US-09-843-930A-1	Sequence 1, Appli
18	998.5	23.7	2151	4	US-09-489-039A-3670	Sequence 3670, Ap
19	915.5	21.7	2843	4	US-09-463-238-1	Sequence 1, Appli
20	915.5	21.6	2843	4	US-09-463-238-10	Sequence 10, Appli
21	810	19.2	2334	5	PCT-US95-09323-1	Sequence 1, Appli
22	810	19.2	2334	5	PCT-US95-09323-1	Sequence 1, Appli
23	807	19.2	2244	1	US-08-476-519-10	Sequence 10, Appli
24	807	19.2	2244	1	PCT-US95-09323-10	Sequence 10, Appli
25	804.5	19.1	2625	6	5457037-4	Patent No. 5457037
26	804.5	19.1	3336	6	5457037-1	Patent No. 5457037
27	781	18.5	1671	4	US-09-252-991A-8261	Sequence 8261, Ap
28	779.5	18.5	2253	6	5457037-2	Patent No. 5457037
29	652	15.5	2523	2	US-08-410-784A-3	Sequence 3, Appli
30	544.5	12.9	2781	4	US-09-313-677-1	Sequence 1, Appli
31	544.5	12.9	2781	4	US-09-514-599-3	Sequence 3, Appli
32	544.5	12.9	2799	4	US-09-313-677-18	Sequence 18, Appli
33	544.5	12.9	7026	4	US-09-313-677-20	Sequence 20, Appli
34	544.5	12.9	7344	4	US-09-313-677-16	Sequence 16, Appli
35	519	12.3	2319	4	US-09-134-078-14	Sequence 14, Appli
36	516	12.3	2766	4	US-09-514-599-1	Sequence 1, Appli
37	506.5	12.0	2784	1	US-08-474-140-10	Sequence 10, Appli
38	506.5	12.0	2784	1	US-08-477-630-10	Sequence 10, Appli
39	506.5	12.0	2784	1	US-08-472-293-10	Sequence 10, Appli
40	506.5	12.0	2784	1	US-08-474-545-10	Sequence 10, Appli
41	506.5	12.0	2784	1	US-08-478-341-10	Sequence 10, Appli
42	506.5	12.0	2784	3	US-08-996-733-10	Sequence 10, Appli
43	506.5	12.0	4464	1	US-08-474-140-8	Sequence 8, Appli
44	506.5	12.0	4464	1	US-08-474-140-9	Sequence 9, Appli
45	506.5	12.0	4464	1	US-08-477-630-8	Sequence 8, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-731-166-15  
; Sequence 15, Application US/09731166  
; Patent No. 6639126  
; GENERAL INFORMATION:  
; APPLICANT: Sewalt, Vincent J. H.  
; APPLICANT: Singletary, George W.  
; TITLE OF INVENTION: Production of Modified Polysaccharides  
; FILE REFERENCE: 35718/206348  
; CURRENT APPLICATION NUMBER: US/09/731,166  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: 60/169,993  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 2700  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Sul isoamylase -- Genbank Accession No. 6639126 AF030882  
; NAME/KEY: CDS  
; LOCATION: (88) ... (2457)  
US-09-731-166-15

Alignment Scores:  
Pred. No.: 0  
Score: 2569.50  
Percent Similarity: 90.28%  
Best Local Similarity: 84.59%  
Query Match: 84.75%  
DB: 4  
Length: 2700  
Matches: 653  
Conservative: 44  
Mismatches: 65  
Indels: 10  
Gaps: 4

US-09-674-817B-3 (1-764) x US-09-731-166-15 (1-2700)





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 Db 1221 TAATTAATCTGCTGTGTGGAAATACCTTCAATGTAATCATCTCTAGTCCGTGAATTAAT 1280  
 QY 374 eValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLe 394  
 Db 1281 AGTGGAATCTCTGAGATACCTGGTAACGAAGAATGCTGTTGATGGTTTTCGTTTGACCT 1340  
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 Db 1341 TGCATCTATCTAGCAGAGGATGAGTCTATGGATCCAGTCAATGTAATGTGTATGGAAGTCC 1400  
 QY 414 cIleGluGlyAspMetIleThrGlyThrProLeuValThrProLeuIleAspMe 434  
 Db 1401 AATGGAGGTGACATGATACACAGGAGGACCTCTTGTTCGCCACCATTTATTTGACAT 1460  
 QY 434 tIleSerAsnAspProIleLeuGlyGlyValIleLeuLeuAlaGluAlaTrpAspAlaGl 454  
 Db 1461 GATTAGCAATGACCAATCTTGGAAATGTCAAGCTCATTTGCTGAAGCATGGGATGCAGG 1520  
 QY 454 yGlyLeuTyrGlnValGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLy 474  
 Db 1521 AGCTCTCTATCAAGAGGTGAGTCTTCCCTCAGTGGAACTTTGGTCAGATGGAAATGAAA 1580  
 QY 474 sTyrArgAspIleValArgGlnPheIleLeuGlyThrAspGlyPheAlaGlyGlyPheAl 494  
 Db 1581 GTATCGCATACCGTGGCTGCTCATCAAGGACACAGATGATTTGCTGCTGCTTTGTC 1640  
 QY 494 aGluCysLeuGlySerProHisLeuTyrGluAlaGlyValArgLysProTrpHisSe 514  
 Db 1641 TGAATGCCCTATGGAAGTCCACAGTTATACAGGAGGGGGAGGAGCTTGCGACAG 1700  
 QY 514 rIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLy 534  
 Db 1701 TATCGCTTTGTATGTGCACACAGTGGATTTACACTGGCTGATTTGGTCACATACATAG 1760  
 QY 534 sIlyTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTr 554  
 Db 1761 CAAGTACAATCTTGTCAATGTTGAGGACTTCAGAGATGGGAAATCATATCTTAGCTG 1820  
 QY 554 pAsnCysGlyGluGlyGluPheAlaArgLeuSerValIysArgLeuArgLysArgGl 574  
 Db 1821 GAATTTGGGGAGGAGGAGGATTTGCAAGTCTGTCTCGAAGATTAAAGGAAGGCA 1880  
 QY 574 rMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGl 594  
 Db 1881 AATGGCAATTTCTTTGTTTGTCTTATGGTTTCTCAGGGAGTTCCAAATGTTCTACATGGG 1940  
 QY 594 yAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrVa 614  
 Db 1941 CGATGAATATGTGTACACAAAGGGAGGAGCAACAATACGTACTGCCATGACCATTAATGT 2000  
 QY 614 lAsnTyrPheArgTrpAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCy 633  
 Db 2001 CAATTAATTTCCGTTGGGTAAGAGAGAGAAACAATCTCTGATTTGTACAGATTCTCGCG 2060  
 QY 633 sLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAl 653  
 Db 2061 TCTCATGACCGAATTCGCAAGAAATGTGAATCTCTTGGCCTTGAGGACTTCCCGACTTC 2120  
 QY 653 aIysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerAr 673  
 Db 2121 AGAACGGTTGAAATGGCAGGTCATCAGCCCGGAGGAGCTGACTGGTCAGAGGCAAGCCG 2180  
 QY 673 gPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnTh 693  
 Db 2181 ATTGTTGCTTCCATGAGGAGGAGCAACCAAGAGGAGAGATCTACGTGGCTTCAACAC 2240  
 QY 693 rSerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgTrpGluProVa 713  
 Db 2241 CAGTCACCTTCCGGTGGTGTGTTGGGCTTCCAGAGCGCTCTGGGTCCGATGGGAGCGGT 2300

QY 713 lValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAl 733  
 Db 2301 GGTGGACACCGGCAAGGAGGACCATATGACTTCTCCTCCGATGGCTGCCAGATCGTGC 2360  
 QY 733 aLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTy 753  
 Db 2361 TGTACCGCTCTACAGTCTCTCATTTCTCACTCCATCTCATCTATCTATGCTCAGCTA 2420  
 QY 753 rSerSerValIleLeuValLeuArgProAspVal 764  
 Db 2421 CTCCTCCATCATCTCTTGTATGGCCCTGATGC 2454  
 RESULT 3  
 US-09-463-238-2  
 ; Sequence 2, Application US/09463238  
 ; Patent No. 6469230  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edwards, Elizabeth A  
 ; APPLICANT: Smith, Alison M  
 ; APPLICANT: Bustos Guillen, Regla  
 ; APPLICANT: Martin, Catherine R  
 ; APPLICANT: Plant Bioscience Limited  
 ; TITLE OF INVENTION: Search Debranching Enzymes  
 ; FILE REFERENCE: 97.118  
 ; CURRENT APPLICATION NUMBER: US/09/463,238  
 ; CURRENT FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB98/02280  
 ; PRIOR FILING DATE: 1998-07-30  
 ; PRIOR APPLICATION NUMBER: GB 9716185.5  
 ; PRIOR FILING DATE: 1997-07-31  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 2706  
 ; TYPE: DNA  
 ; ORGANISM: Solanum tuberosum  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (2641)  
 ; OTHER INFORMATION: n = a o r g o r c o r t  
 US-09-463-238-2  
 Alignment Scores:  
 Pred. No.: 0 Length: 2706  
 Score: 3029,00 Matches: 546  
 Percent Similarity: 81.57% Conservative: 78  
 Best Local Similarity: 71.37% Mismatches: 113  
 Query Match: 71.91% Indels: 28  
 DB: 4 Gaps: 7  
 US-09-674-817B-3 (1-764) x US-09-463-238-2 (1-2706)  
 QY 10 TrpArgPro-----AspAlaThrAlaGlyLysGlyValGlyGluVal 23  
 Db 178 TGGAGAAATCCAGCTCTTCAGTGGTTTANCTGCTTTCATAGTACGAGCTGGTGG 237  
 QY 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluGluAspGluPro 43  
 Db 238 -----GTGAAGACTGGCGCTACTGCGTGGTGGAG-----AAGCGG 276  
 QY 44 ValAlaGluAspArgTyrAlaLeuGlyValAlaCysArg-----ValLeuAlaGlyMet 61  
 Db 277 ACGACGGA-----CGATGCTGTTTTCAGGTTTATCAGGAGAG 315  
 QY 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValValAsnPheAlaValTyrSerGly 81  
 Db 316 CCATTGCGGTTTGGTGTCTACTGCGACAGATGGTGGTGAATTCGCTGTTTTTCAAGG 375  
 QY 82 GlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101  
 Db 376 AATGCTACAGCTGTCTCTTTGCTTGTACATCTTTCCGATTTCCTTCCGAGAGAGAGTG 435



QY 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTyrHisValPhe 121  
DB 436 ACCGAGCAAAATTTTCCTGGATCTCTAGCTAATAAAACCTGAGATGATGGCATGTCTC 495  
QY 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141  
DB 496 CTTAAGGAGATTTTGAGATATCTATATGGCTACAAATTTGATGGAAATTTCTGTCT 555  
QY 142 HisCysGlyHisTyrLeuAspValSerAsnValValValAspProTyrAlaLysAlaVal 161  
DB 556 GAAGAAGACACTACTTTGACTCTTCGAGATAGTGTGGATCTTATGTCAGGCTATA 615  
QY 162 IleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTyrProGlnMetAla 181  
DB 616 GTAAGCAGAGAGAATATGGTGTATTAGGGCCAGAGGATGATTGTGGCCCCCAATGGCT 675  
QY 182 GlyMetIleProLeuProTyrSerThrPheAspTyrGluGlyAspLeuProLeuArgTyr 201  
DB 676 GGCATGGTACTCTCTGCTCTGATCAGTTTGTATGGGAGAGATCTACCACTGAAGTTT 735  
QY 202 ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSer 221  
DB 736 CCACAGAGATCTTTGTAATCTATGAATGATGATGCTGGTGTGGAGAACTTGATCACTTGAAG 855  
QY 222 SerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLysLeuAspTyrLeuLys 241  
DB 796 AGTCAACAAATACTCTGTTACTTCTGTTGGTGTGGAGAACTTGATCACTTGAAG 855  
QY 242 GluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyr 261  
DB 856 GAACTTGGTCAACTATAGAGCTAATGCCCTGTCCAGAGTTCATGAGCTGGAGTAC 915  
QY 262 SerThrSerSerSer-----LysMetAsnPheTyrGlyTyrSerThrIle 276  
DB 916 TATAGTTATTAACCTGATTGGGCGACTACAAATTTAACTTTTGGGGCTAATCTACTGTC 975  
QY 277 AsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAsp 296  
DB 976 AATTTCTTTTCCAAATGGGAAGATCTCATCTGCTGGTCTAGTAAATTTGGGGCTCGGT 1035  
QY 297 AlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIle 316  
DB 1036 GCAATAAAGCAATTTAAGTATCTTGTCAAGGAAGCACATAAAGCTGGAATCGAGGTTATC 1095  
QY 317 LeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPhe 336  
DB 1096 ATGATGTGTCTTCAATCACACTGCTGAAGGAATGAAATGGTCCCATATCTATCATTT 1155  
QY 337 LysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyr 356  
DB 1156 AGAGGCATGACAAACAGTGTGTTTATACGCTAGCTCTTAAGGGTGAATTTTACAACATAC 1215  
QY 357 SerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAsp 376  
DB 1216 TCAGGAATGGAAATACCTTCACTGTAATATATCCATTTGATGCTGCTGCTTCTCTCT 1275  
QY 377 CysLeuArgTyrTyrValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSer 396  
DB 1276 TGCTTGAGATATTTGGGTATCCGAAATGCAGTAGATGGCTTCGGCTTGAATCTTCTCTCT 1335  
QY 397 IleMetThrArgGlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGlu 416  
DB 1336 ATCCCTTACAAAGAGTAGCAGCTGCTGGAATGCTGTAATGCTATGGAATTCATTCATGC 1395  
QY 417 GlyAspMetIleThrThrThrProLeuValThrProLeuIleAspMetIleSer 436  
DB 1396 GGTGAGGTGATCCACAGGCTCTCTCAAGCCCAACCATGATGATGATGATGATGATGATG 1455  
QY 437 AsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTyrAspAlaGlyGlyLeu 456  
DB 1456 AATGATCCAAATCTCTGCTGGAGTAAAGCTTATAGCTGAAGCATGGATGTTGGAGGCTT 1515  
QY 457 TyrGlnValGlyGluPheProHisTyrAsnValTyrSerGluTyrAsnGlyLysTyrArg 476

DB 1516 TACCAAGTTGGCATGTTTCCGCACCTGGGTATCTGGTCGAGTGGACCGAAGTACCGT 1575  
QY 477 AspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCys 496  
DB 1576 GACATGCTACGGCAGTTCATCAAGGCACTGATGGTTTTCGTGGGCTTTTCTGTAATGC 1635  
QY 497 LeuCysGlySerProHisLeuTyrGlnAlaGlyArgLysProTyrHisSerIleAsn 516  
DB 1636 CTTTGGGAAGCCCAATCTATACCAAGAAAGGAGAAACCAATGAGCAAGTATAAT 1695  
QY 517 PheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyr 536  
DB 1696 TTTGCTGTGGCCACGATGTTTACTTTGGCTGATTTAGTGACATACACANTAAACAC 1755  
QY 537 AsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrPheAsn 556  
DB 1756 AATTTGGCAAAATGGAGAGGACCAACAAAGACGGGAGAAATCAATAATAGTTGGAATGT 1815  
QY 557 GlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArg 576  
DB 1816 GGTGAGGAAGGAGATTTTGCAGATATCTTTGTGAAGAAATTTGAGGAAAGACAAATGCGG 1875  
QY 577 AsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGlu 596  
DB 1876 AACTTCTCTCTGCTTATGTTTCCCAAGTGTTCATGATATATATGGCGATGAA 1935  
QY 597 TyrGlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyr 616  
DB 1936 TATGCTCACATAGGGAGGAAACCAACACACGATTTGCCATGATATAATTAATATAC 1995  
QY 617 PheArgTyrAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 635  
DB 1996 TTTCCGTTGGGATAGAGAGATCTTCTCTCTGATTTTGGATTTTGGGCTCATG 2055  
QY 636 ThrLysPheArgLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 655  
DB 2056 ACCAAATTTCCGCCATGATGTAATCTAGTGGATTTAGTGGTTTCCCTTACAGCAGAAAG 2115  
QY 656 LeuGlnTyrHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArgPheVal 675  
DB 2116 CTGCAATGGCATGTCACATCTCTAGAACTCCAGATTTGGTCTGAAACAAATGCTGTT 2175  
QY 676 AlaPheSerMetLysAspGluArgGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 695  
DB 2176 GCATTCACATGTCGACAAAGTGAAGGAGAACTATATATTTGCTTTTAAAGCCAGCAT 2235  
QY 696 LeuProAlaValValGluLeuProGluArgAlaGlyArgArgTyrGluProValValAsp 715  
DB 2236 TTGGCTGTACGATTAACATCTCCAGATAGGCTGGTGTATAGATGGCAGCGCTTTGTGGAC 2295  
QY 716 ThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThr 735  
DB 2296 ACAGGCAAAACAGCACCATTGACTTCTTGACAGCAGCTTCTCTGAGAGAGACAGCA 2355  
QY 736 IleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSer 755  
DB 2356 GCCAAACAAATTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2415  
QY 756 ValIleLeuValLeu 760  
DB 2416 ATTATTTCTTTACTA 2430

## RESULT 4

US-09-463-238-11  
; Sequence 11, Application US/09463238  
; Patent No. 6469230  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Elizabeth A  
; APPLICANT: Smith, Alison M  
; APPLICANT: Bustos Guillen, Regla  
; APPLICANT: Martin, Catherine R  
; APPLICANT: Plant Bioscience Limited

```

; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463,238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: GB 9716185.5
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (822, 826, 2707 and 2797)
; OTHER INFORMATION: n = a or g or c or t
US-09-463-238-11

Alignment Scores:
Pred. ID.: 0 Length: 2806
Score: 2923.00 Matches: 538
Percent Similarity: 80.23% Conservative: 79
Best Local Similarity: 69.96% Mismatches: 119
Query Match: 69.40% Indels: 33
DB: 4 Gaps: 9

US-09-674-817B-3 (1-764) x US-09-463-238-11 (1-2806)
QY 10 TrpArgPro-----AsnAlaThrAlaGlyysGlyValGlyGluVal 23
Db 241 TGGAGAAAATCGAGGTCTTCAGTGGTTAAATGCTGCTTCATAGTGGACCGTGGAGGTG 300
QY 24 CysAlaAlaValValGluAlaAlaThrLysValGluAspGluGlyGluAspGluPro 43
Db 301 -----GTGAGACTCGGGCTACTCGCGTGGTGGTGGAG-----AAGCCG 339
QY 44 ValAlaGluAspArgTyrAlaLeuGlyGlyAlaCysArgVal-----LeuAlaGlyMet 61
Db 340 ACGACGGAA-----CGATGCTGTTTGGAGTTTATACGGGAAAG 378
QY 62 ProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSergly 81
Db 379 CCAITGGCGTTGGTGTCTACTCGACAGATGGTGGTGAATTCGCTGTTTTCAGGA 438
QY 82 GlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgVal 101
Db 439 AATGCTACAGCTGCTACTCTTTGCTTGATCCTCTTTCCGATTTACCTCGAAGAGAGTG 498
QY 102 ThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPhe 121
Db 499 ACCGAGCAATTTCTCGATCTCTCTAGCTAAATAAACTGGAGATGATGGCATGTGTC 558
QY 122 IleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaPro 141
Db 559 CTTAAGGAGAGATTTTGAGAAATATGCTATATGGCTACAAATTTGATGGGAAATTTCTGCT 618
QY 142 HisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAlaLysAlaVal 161
Db 619 GAAGAGGACACTTCTTGATCTCTTCAGATAGTGTGGATCTTATGCCAAGGCTATA 678
QY 162 IleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGluMetAla 181
Db 679 GTAAGCAGAGAGAAATATGTTGATTTAGGGCCAGAGGATGATTTGTTGGCCCAATGGCT 738
QY 182 GlyMetIleProLeuProTyr---SerThrPheAspTrpGluGlyAspLeuProLeuArg 200
Db 739 GGCATGGTACCCTTCTGCTCTCGATCAGTTTGTATTTGGAGAGAGATCTACCACTCGAA 798
QY 201 --TyrProGluLysAspLeuVal-IleTyrGluMetHisLeuArgGlyPheThrLysHis 219
Db 799 GTTTCCACAGAGAGATCTTGTTCATCNCATGAAATGATGATGTTCTGTTGGTTTACTATCCAT 858

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QY 220 AspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyr 239
Db 859 GAGTCGAGTGAACAAAATATCTGGTACTTACTCTTGGTGTGGAGAACTTGTATCAT 918
QY 240 LeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeu 259
Db 919 TTGAAGGAACCTTGGTGTCAACTGTATAGAGCTAATGCCCTGTACAGAGTTCATAGCTG 978
QY 260 GluTyrSerThrSerSerSer-----LysMetAsnPheTrpGlyTyrSer 274
Db 979 GAGTACTATAGTTATAACTCTGTATTGGGCGACTACAAGTTTAACTTTTGGGGCTATCT 1038
QY 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294
Db 1039 ACTGTCAATTTCTTTTCTCCAATGGGAAGATATCTATCTGCTGGTCTAAGTAATTCGCG 1098
QY 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314
Db 1099 CTCGGTCCATAAACGAATTTAAGTATCTTGTCAAGAGAGCACATAAAGCTGGAATCGAG 1158
QY 315 ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu 334
Db 1159 GTTATCATGATGTGTTTTCATCATCACTGCTGGAAGAAATGAAATGCTCCCATCTATA 1218
QY 335 SerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyr 354
Db 1219 TCATTTAGAGGCAATGACACACAGTGTGTTTATACGCTAGCTCCTAAGGSGTGAATTTAC 1278
QY 355 AsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIle 374
Db 1279 AACTACTCAGAGTGTGGAATATCTTCAATGTGTAATATCCCATTTGACGTCAATTTATA 1338
QY 375 ValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeu 394
Db 1339 GTG---ATGCTGAGATATTTGGTGTACCGAATACGAGTACATGGCTTCGCTTTCATCTT 1395
QY 395 AlaserIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaPro 414
Db 1396 GCTTCTATCTCTACAAAGAGTAGCAGCTCGTGGAAATGCTGTAAATGTCTATGAAATTTCA 1455
QY 415 IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProLeuIleAspMet 434
Db 1456 ATTGACGGTACGTGATCACCACAGGCACTCTCTCACAGGCCCATTTGATGATG 1515
QY 435 IleSerAsnAspProIleLeuGlyValLysLeuIleAlaGluAlaTrpAspAlaGly 454
Db 1516 ATTAGCAATGATCCAATATCTCTGGAGTAAAGCTTATAGCTGAAGCATGGGATTTGGA 1575
QY 455 GlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLys 474
Db 1576 GGCCTTTACCAAGTTGGCATGTTTCCGCACTGGGTATCTGTCGGAGTGGACGGAAG 1635
QY 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAla 494
Db 1636 TACCGTCACATGTGTAGCGCAGTTCATCAAGGCACTGATGGGTTTCTTCTGGGCTTTTCT 1695
QY 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyValArgLysProTrpHisSer 514
Db 1696 GAATGCTTTGTGGAGGCCCAATCTATACCAAGAAAGGAGGAGAAACCATGGACAGT 1755
QY 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534
Db 1756 ATAAATTTCTGTGTGCCCACTGTTTACTTTTGGCTGATTTAGTGACATACACCAAT 1815
QY 535 LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrp 554
Db 1816 AAACACAAATTTGCAATGGAGGAGACACAAAGACGGGGAATTCACAAATAATGTTGG 1875
QY 555 AsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln 574
Db 1876 AATTGTGGTGGAGAGAGATTTTGCAGTATCTTGTGTAAGAAATTTGAGGAAAGACAA 1935

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QY 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594
DB 1936 ATGCGGAATCTTCTCTGCTTATGCTTCCCAAGGTGTCCTCATGATATATATGGC 1995

QY 595 AspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrVal 614
DB 1996 GATGATATATGTCACATTAAGGAGGAAACACACACGATATGCCATGATAAATATAT 2055

QY 615 AsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys 633
DB 2056 AATTACTTCCCTGGGATAAGAGGATGAATCTTCACTCTGATTTTTCAGATTTTGGCGC 2115

QY 634 LeuMetThrLysPheArgLysGlyCysGluCylLeuGlyLeuGluAspPheProThrAla 653
DB 2116 CTCATGACCAATTCGCGCCATGAATGAATCACTGGGATTAGATGTTTCCCTACAGCA 2175

QY 654 LysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArg 673
DB 2176 GAAAGGCTGCAATGGCATGTCACACTCCAGACTCCAGATTGGTCTGAAACAGTCGA 2235

QY 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnThr 693
DB 2236 TTCCTTGCAATTCACACTGGTCGACAAAGTCAAGGAGAACTATATATGCTTTAACGCC 2295

QY 694 SerHisLeuProAlaValGluLeuProGluArgAlaGlyArgTyrProGluProVal 713
DB 2296 AGCAATTGCTGTAAACGATTACACTTCCAGATAGGCTGTTATAGATGGCAGCCGTT 2355

QY 714 ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla 733
DB 2356 GTGACACACAGCAAAACAGCACCATTGACTTCTTGACAGCAGCTTCTGAGAGAGAG 2415

QY 734 LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr 753
DB 2416 ACAGCACCAAAACAAATATCTCAATTTCTGACGCGAACCAGTATCCGATGCTCAGTTAT 2475

QY 754 SerSerValIleLeuValLeu 760
DB 2476 TCATCCATTATCTTTTACTA 2496

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## RESULT 5

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US-09-187-124-1
; Sequence 1, Application US/09187124A
; Patent No. 6255563
; GENERAL INFORMATION:
; APPLICANT: Emmermann, Michael
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; FILE REFERENCE: GFB8
; CURRENT APPLICATION NUMBER: US/09/187,124A
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: PCT/EP97/02292
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: DE 196 18 125.9
; EARLIER FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1819)
; OTHER INFORMATION: Clone: Iso5
US-09-187-124-1

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## Alignment Scores:

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Pred. No.: 2,1e-291 Length: 2133
Score: 2612.00 Matches: 460
Percent Similarity: 86.86% Conservative: 62
Best Local Similarity: 76.54% Mismatches: 73

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Query Match: 62.01% Indels: 7
DB: 3 Gaps: 2
US-09-674-817b-3 (1-764) x US-09-187-124-1 (1-2133)

QY 166 GluTyrGlyValProAlaArgGlyAsnAsnCysTyrProGlnMetAlaGlyMetIlePro 185
DB 1 GAATTCGGCAGGAGCCAGAGGAT--GATTGTTGGCCCCCAATGGCAGCATGGTACCT 58

QY 186 LeuProTyrSerThrPheAspTyrGluGlyAspLeuProLeuArgTyrProGlnLysAsp 205
DB 59 TCTGCTTCTGATCAGTTTGAATGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGAT 118

QY 206 LeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGlu 225
DB 119 CTGTGAATCTAGAAATGATGTTCTGTGATTTTACAATCATGAGTCGAGTGAACAAAA 178

QY 226 HisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyVal 245
DB 179 TATCCTGGTACTTACCTTGGTGTGTGGAGAACTTGTATCACTTGAAGGAACCTTGGTGC 238

QY 246 AsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSer 265
DB 239 AACTGTATAGACTAATGCCCTGTCCAGAGTTCAATGAGCTGAGTACTATAGTTATAAC 298

QY 266 Ser-----LysMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSer 280
DB 299 TCTGTATTGGGCGCATACAAAGTTTAACTTTTGGGCTATTCTACTGTCAATTTCTTTCT 358

QY 281 ProMetThrArgTyrThrSerGlyGlyLysAsnCysGlyArgAspAlaIleAsnGlu 300
DB 359 CCAATGGGAAGATCTCTGCTGCTCTAAGTAAATTCGGGCTCGGTGCAATAACGAA 418

QY 301 PheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal 320
DB 419 TTTAAGTATCTGTCAAGAGACCATTAACGTGAATCGAGTTTATCATGATGTTGTT 478

QY 321 PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuValAspCysLeuArgTyr 340
DB 479 TTCAATCACACTGCTGAAGGAAATGAAATGCTCCATCTATCATTTAGAGGCATTGAC 538

QY 341 AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly 360
DB 539 AACAGTGTTTATACGCTAGCTCCTAAGGTTGAATTTTACAACTACTCGGATGTGGA 598

QY 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
DB 599 AATACCTTCAACTGTATAATCCCATTTGATCGTCAATTTATAGTGGATTGCTTGAGAT 658

QY 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
DB 659 TGGGTTACCGAAATGCACGTAGTGGCTTCCGCTTTGATCTTGTCTTCTATCTTACAGA 718

QY 401 GlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
DB 719 AGTAGCAGCTCGTGAATGCTGTAATGCTCTATGGAATTCATTTGACGGTGCATGATC 778

QY 421 ThrThrGlyThrProLeuValThrProLeuIleAspMetIleSerAsnAspProIle 440
DB 779 ACCAGGCACCTCTCTCAAGGCCACCATTTGATTGATATGATTAGCAATGATCCATA 838

QY 441 LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGly 460
DB 839 CTTAGTGGATTAAGCTTATAGCTGAAGCATGGGATTGTGAGGCCCTTTTCAAGTTGGC 898

QY 461 GlnPheProHisTrpAsnValTrpSerGluTyrAsnGlyLysTyrArgAspIleValArg 480
DB 899 ATGTTTCCGCACTGGGTATCTGTGCGAGTGGAAACGGAAGTACCGTGCATGATGTTAC 958

QY 481 GlnPheIleLysGlyThrAspGlyPheAlaGlyClyPheAlaGluCysLeuCysGlySer 500
DB 959 CAGTTTCAACAAAGCAGTGAATGGGTTTCTGGGGCTTTTGTGTAATGCCCTTTGTGAAGC 1018

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501 ProHisLeuTyr-GlnAlaGlyGlyArgLysProThrHisSerIleAsnPheValCysAla 520  
1019 CCAATCTATACCAAGAGGAGGAGAGAAACCATGGAACAGTATATAATTTCTGTGTGCC 1078  
521 HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn 540  
1079 CACGATGGTTTACTTTGGCTGATTTAGTGATACACAAATAACAAACAATTTGGCAAT 1138  
541 GlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrAsnCysGlyGluGluGly 560  
1139 CGAGGAGGACAAAGAGATGGGAGATCACATAATAGTTGGATTTGGCGAGGAGGA 1198  
561 GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal 580  
1199 GAATTGGCAAGTATCTTTGTGAAGAAATGAGGAAAGACAAATGCGGAATCTTCTCTC 1258  
581 CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr 600  
1259 TGCCTATGTTTCCCAAGGTTCCTCATGATATATATATGATGATGATGATGATGAT 1318  
601 LysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAsp 620  
1319 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1378  
621 LysLys--GluGlnTyr-SerGluLeuHisArgPheCysCysLeuMetThrLysPheArg 639  
1379 AAGAGGATGATCTTCTCATCTGATTTTGTGATTTTGGCGCTCATGACCAATTCGCG 1438  
640 LysGluCysGlyGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTyrHis 659  
1439 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1498  
660 GlyHisGlnProGlyLysProAspThrSerGluAsnSerArgPheValAlaPheSerMet 679  
1499 GGTACACTCTAGAACTCCAGATGGTCTGAAACAGTGCATGCTGATTTACACTG 1558  
680 LysAspGluArgGlnGlyGluLeuTyrValAlaPheAsnThrSerHisLeuProAlaVal 699  
1559 GTGCAGAAAGTGAAGGAGAGACTATATATGCTTTTAAACGACGACCAATTTGCTG 1618  
700 ValGluLeuProGluArgAlaGlyArgTyrProValValAspThrGlyLysPro 719  
1619 ATTACACTTCCAGAAAGCTGGTATAGATGGCAGCGGTTTGGACACAGGCAACCA 1678  
720 AlaProTyrAspPheLeuThrAspLeuProAspArgAlaLeuThrIleHisGlnPhe 739  
1679 GCACCATTTGACTTCTGACAGCAGATGTTCTCTGAGAGAGAGACAGCAGCAGCAATAT 1738  
740 SerHisPheLeuTyr-SerAsnLeuTyr-ProMetLeuSerTyrSerSerValIleLeuVal 759  
1739 TCTCATTTCTGGACGCGAACAGTATCCGATGCTCAGTTATTCATCCATATCTTTTA 1798  
760 Leu 760  
1799 CTA 1801

## RESULT 6

US-09-850-936-1  
Sequence 1, Application US/09850936  
Patent No. 670525  
GENERAL INFORMATION:  
APPLICANT: Emmermann, Michael  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES  
TITLE OF INVENTION: FROM POTATO  
FILE REFERENCE: GFB8  
CURRENT APPLICATION NUMBER: US/09/850,936  
CURRENT FILING DATE: 2001-05-08  
PRIOR APPLICATION NUMBER: US/09/187,124  
PRIOR FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: PCT/EP97/02292  
PRIOR FILING DATE: 1997-05-06  
PRIOR APPLICATION NUMBER: DE 196 18 125.9

PRIOR FILING DATE: 1996-05-06  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2133  
TYPE: DNA  
ORGANISM: Solanum tuberosum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)..(1819)  
OTHER INFORMATION: Clone: Iso5  
US-09-850-936-1  
Alignment Scores:  
Pred. No.: 2,1e-291 Length: 2133  
Score: 2612.00 Matches: 460  
Percent Similarity: 86.86% Conservative: 62  
Best Local Similarity: 76.54% Mismatches: 73  
Query Match: 62.01% Indels: 7  
DB: 4 Gaps: 2  
US-09-674-817B-3 (1-764) x US-09-850-936-1 (1-2133)  
QY 166 GluTyrGlyValProAlaArgGlyAsnAsnCysTyrProGlnMetAlaGlyMetIlePro 185  
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QY 186 LeuProTyrSerThrPheAspTyrGluGlyAspLeuProLeuArgTyrProGlnLysAsp 205  
Db 59 TCTGCTTCTGATCATGTTGATTGGGAAGGAGATCTTATTACTGAAGTTTCCACAGAGAT 118  
QY 206 LeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGlu 225  
Db 119 CTGTATATCTGAAATGATGTTCTGGGATTTACAAATCATGAGTCGATGAAACAAA 178  
QY 226 HisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuVal 245  
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QY 246 AsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSer 265  
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QY 266 Ser-----LysMetAsnPheTyrGlyTyrSerThrIleAsnPheSer 280  
Db 299 TCTGATTTGGCGACATACAAAGTTTAACTTTGGGGCTATTTACTGTCAATTTCTTTCT 358  
QY 281 ProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGlu 300  
Db 359 CCAATGGGAAGATACCTGCTGCTGCTAAGTAAATGGTCCCTCGGCTCGGTCAATAACGAA 418  
QY 301 PheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal 320  
Db 419 TTTAAGTATCTTGTCAAGGAGACATAACCGTGAATCGAGTTTATCATGATGTTGT 478  
QY 321 PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp 340  
Db 479 TTTCAATCAGCTCTGAGAGGAATGAAATGGTCCCTACTATCATTTAGAGCATTCAC 538  
QY 341 AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly 360  
Db 539 AACAGTGTGTATATACGCTAGCTCTTAAGGGTGAATTTTCAACTACTCAGAGTGTGA 598  
QY 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380  
Db 599 AATACCTTCACTGTAATATCCATTTGATGCTCAATTTATAGTGGATTTGATGATAT 658  
QY 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400  
Db 659 TGGGTATACCGAAATGACACGTAGATGCTTCCCGCTTTGATCTTCTTATCTTCAAGA 718  
QY 401 GlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420

Db 719 AGTAGCAGCTGCTGGAATGCTTAATGCTATGCAAAATTCATGAGGTGACATGATC 778  
QY 421 ThrThrGlyThrProLeuValThrProProLeuLeuAspMetIleSerAsnAspProle 440  
Db 779 ACCACAGGCACTCTCTCACAGCCCACTTATGATGATGATGATGATGATGATGATGAT 838  
QY 441 LeuGlyGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 460  
Db 839 CTTAGTGGAGTAAAGCTTATAGCTGAGCATGGGATTTGTGGAGCCCTTTACCAAGTTGGC 898  
QY 461 GlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTrpArgAspIleValArg 480  
Db 899 ATGTTTCCGCAGCTGGGTATCTGCTGGAGTGGAAAGCAAGTACCCTGACATGGTACGT 958  
QY 481 GlnPheLeuLeuGlyThrAspGlyPheAlaGlyPheAlaGluCysLeuCysGlySer 500  
Db 959 CAGTTCAATCAAGGCACTGATGGGTTTCTGGGCTTTTGTGAATGCCCTTTGGGAAGC 1018  
QY 501 ProHisLeuTrpGlnAlaGlyArgLysProTrpHisSerIleAsnPheValCysAla 520  
Db 1019 CCAAAATCTATACCAAGAGGAGGAGAAACCATGGAACAGTAAATTTCTGTGTGCC 1078  
QY 521 HisAspGlyPheThrLeuAlaAspLeuValThrTrpAsnLysLysTrpAsnLeuProAsn 540  
Db 1079 CACGATGGTTTACCTTGGCTGATTTAGTACATACAAATTAACCAATTTGGCAAT 1138  
QY 541 GlyLeuAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGly 560  
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QY 561 GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal 580  
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QY 581 CysLeuMetValSerGlnGlyValProMetPheTrpMetGlyAspGluTrpGlyHisThr 600  
Db 1259 TGCCTTATGCTTCCCAAGTCTCCCATGATATATATGCGTGATGAATGCTGCACACT 1318  
QY 601 LysGlyGlyAsnAsnAsnThrTrpCysHisAspSerTrpValAsnTrpPheArgTrpAsp 620  
Db 1319 AAGGAGGAGAAACAAACACAGTATGCGCATGCAATATATATTAATTAATTTCCGTTGGAT 1378  
QY 621 LysLys--GluGlnTrpSerGluLeuHisArgPheCysCysLeuMetThrLysPheArg 639  
Db 1379 AAGAAGATGATCTTCATCTGATTTTGTAGATTTTGGCGCTCATGCCAAATTCGC 1438  
QY 640 LysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHis 659  
Db 1439 CATGAATGTGAATCACTGGGATATAGATGTTTCCCTACAGCAGAAAGCTGCAATGCCAT 1498  
QY 660 GlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMet 679  
Db 1499 GGTCACTCTTAGAATCCAGATTTGGTCTGAACAACTCGATTCGTTGCATTTACACTG 1558  
QY 680 LysAspGluArgGlnGlyLeuLeuTrpValAlaPheAsnThrSerHisLeuProAlaVal 699  
Db 1559 GTCCGAAAGTGAAGGAGAACTATATATGCTTTAAGCGCCCACTTTGCTGTGAACG 1618  
QY 700 ValGluLeuProGluArgAlaGlyArgTrpGluProValValAspThrGlyLysPro 719  
Db 1619 ATTACACTCCAGAAAGCGCTTATAGATGGCAGCGCTTTGTGGACAGGCAACACCA 1678  
QY 720 AlaProTrpAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPhe 739  
Db 1679 GCACCATTTTGAATCTCTGACAGCAGTATTCCTGAGAGAGAGACAGCAGCCAAACAATAT 1738  
QY 740 SerHisPheLeuTrpSerAsnLeuTrpProMetLeuSerTrpSerValIleLeuVal 759  
Db 1739 TCTCATTTTCTGGACGCGAACCAGTATCCGATGCTCAGTTATTCATCAATTTCTTTTA 1798  
QY 760 Leu 760  
Db 1799 CTA 1801

## RESULT 7

US-09-463-238-3  
; Sequence 3, Application US/09463238  
; Patent No. 6469230  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Elizabeth A  
; APPLICANT: Smith, Alison M  
; APPLICANT: Bustos Guillen, Regla  
; APPLICANT: Martin, Catherine R  
; APPLICANT: Plant Bioscience Limited  
; TITLE OF INVENTION: Starch Debranching Enzymes  
; FILE REFERENCE: 97.118  
; CURRENT APPLICATION NUMBER: US/09/463,238  
; CURRENT FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/02280  
; PRIOR FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: GB 9716185.5  
; PRIOR FILING DATE: 1997-07-31  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2634  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
US-09-463-238-3

## Alignment Scores:

Pred. No.: 1,55e-171 Length: 2634  
Score: 1577.00 Matches: 329  
Percent Similarity: 58.90% Conservative: 111  
Best Local Similarity: 44.04% Mismatches: 235  
Query Match: 37.44% Indels: 72  
DB: 4 Gaps: 19

US-09-674-817B-3 (1-764) x US-09-463-238-3 (1-2634)

QY 30 AlaAlaThrLysValGluAspGluGluAspGluProValAlaGluAspArgTyr 49  
Db 239 GCAGCAGCTAACTTCAGGAAGAGCT-----CCTCAATGCTGCACACTTC 286  
QY 50 AlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAla 69  
Db 287 CCT-----TCATTCAAAGTTTCCCTGCTGCTCATCCACTAGGAGTATCAGAA 337  
QY 70 LeuAlaGlyGlyValAsnPheAlaValTrpHisValPheIleGluGlyGluLeu 89  
Db 338 ACTGAAAGTGAATAAATTTGCAATTTTCTCAGCATGCTTCTGCAGTTACACTTGC 397  
QY 90 LeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAspPro 109  
Db 398 ATAAATCTTCCAAAGAGTGTTCATGATGGAATGATT-----GAATTAGCATGGATCCA 451  
QY 110 LeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyGluLeu-----His 127  
Db 452 CAGAAAGACCCGACAGGAGACATATGGACATATGCAATTAAG---GAGTTGCCCAAGGT 508  
QY 128 AsnMetLeuTrpGlyTrpArgPheAspGlyThrPheAlaProHisCysGlyHisTrpLeu 147  
Db 509 GGTGCTCTTATGTTATCGCATTTGATGGACCTCGAAATGGCATGAAGGCGCATCGATT 568  
QY 148 AspValSerAsnValValAspProTrpAlaLysAlaValIleSerArgGlyGluTyr 167  
Db 569 GATGATAGCATTTTGTGTTGATCCCTTACGCAAACTAATTTGAAGGTCCAGCAGTTT 628  
QY 168 GlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuPro 187  
Db 629 GCA-----GATGAAAGCAATAAAATGTTAGATTTTTGGCACTTATGATTTCAAT 679  
QY 188 TyrSerThrPheAspTrpGluGlyAspLeuProLeu---ArgTyrProGlnLysAspLeu 206  
Db 680 AGCTTGCCTTTTGAATGCGGAGAAATTTCAAGCTTCCAAATATACCAGGAAGATCTT 739

207 ValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHis 226  
 740 GTTATATAGATGAATGTTGCTTTTACTGCTGATGAACAAGTAGTTGGATCAA 739  
 227 Pro-----GlyThrPheIleGlyAlaValSerLysLeuAspTyrLysGluLeuGly 244  
 800 GATCAACGGGGAAGTTACCTTGCTTAAATGAAAGATACACATCTTCTCGAGCTTGGT 859  
 245 ValAsnCysIleGluLeuMetProCysHisIleGluPheAsnGluLeuGluTyr----- 261  
 860 GTCAATGCGAGTASATTAATGCTGTTTGGTTGATGAACTGGAAATACAAAGCGCA 919  
 262 ----SerThrSerSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSer 280  
 920 CCTAATCCGAGATACATGATCAATACATGCGGCTACTCAACAATAAACTTTTGTGCT 979  
 281 ProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsn--- 299  
 980 CCAATGAGTCGATATGCAAGT-----TGTTGGTGGCGGACCTGTCCTGGCT 1024  
 300 -----GluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeu 317  
 1025 TCTCGGAGTTCAAAGAAATGCTCAAGGCTTGCTGATGCTGCGAATGAGTCACTTA 1084  
 318 AspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyPro----IleLeuSerPhe 336  
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 337 LysGlyValAsnThrThrTyrTyrMet-----LeuAlaProLysGlyGluPheTyr 354  
 1145 CGAGGAATAGACAAAGGTTTATACATGTTAGATTTAAACAAATGCTGAGTCTG 1204  
 355 AsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIle 374  
 1205 AATTTCCTGGAGTGGAAATACITTTAACTGCAACCATCCACAGTCATGGAACCTATA 1264  
 375 ValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeu 394  
 1265 CTTGAAAGCTTAAGACCTGGCTCACCAGTATCATGTCGATGATTTGCTTTGATCTT 1324  
 395 AlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaPro 414  
 1325 GCTAGTGTCTTTGCAAGGG----- 1345  
 415 IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMet 434  
 1346 -----ACAGATGGTACTCCCATTAATGCTCCGCCCTTGTAAAGGCC 1387  
 435 IleSerAsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly 454  
 1388 ATTTCGAAGATAGTGTATGTCAGGTGCAAAATATTTGTCGACCATGGGATTTGGA 1447  
 455 GlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLys 474  
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 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyPheAla 494  
 1508 TACCGGATGACATCAGAGATTTATAAGGGCGATGCTGCGATGAAGGAATTTTGA 1567  
 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyArgLysProTrpHisSer 514  
 1568 ACCCGTATCGCAGGTTTCAGCGGATCTGTACAGAGTGAACGAAGCCGCTACCAAGT 1627  
 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534  
 1628 GTCAACTTCGATGTCCTCATGATGGCTTTACCTTGATGACCTTGTTCTCATCAATAT 1687  
 535 LysTyrAsnLeuProAsnGlyCylAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrp 554  
 1688 AAGCAATATGATGCAACCGGTGAAGGTGGCAATGATGATGCAATGCAACATTCAGTTGG 1747  
 555 AsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln 574

1748 AATTGTGGAATTGAAGTGAACCTTCAGATGCAAAATATTAAOCGCACTGCGTTCCACGCCAA 1807  
 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594  
 1808 ATGAAATATTTTCAATTTGGCACTGATGTTTCTCAGGGAACACCAATGATGCTTATGGGG 1867  
 595 AspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrVal 614  
 1866 GATGAGTATGGCATACCCGCTATGGAATAATAACAGITATGACATCATACCGCCATC 1927  
 615 AsnTyrPheArgTrpAspLysLysGluGlnTyrSerGluLeuHis----ArgPheCysCys 633  
 1928 AACAAATTTCCAGTGGGACAAATTTGGAAGCAAGCAAGAAATGATCACTTCAGGTCTTTTCC 1987  
 634 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAla 653  
 1988 AAGATGATAAAGTTTCCGACTGCTCCCAATGTTCTTTAGAAAGGAAACTTCATTGAGAAG 2047  
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 2153 GCACACCACTTCTCCATCAAAACAGCAATACCTTACCACCAAGAAATAGAAATTGGTAC 2212  
 712 ProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAspLeuProAsp 731  
 2213 CGAGTGGTGACACTAATCTGAAATCACCAGATGATTTGTTACTGAGGAGGATGCTGCT 2272  
 732 ArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeu 751  
 2273 -----ATCAGTAAACATTATGATGTTGCG 2296  
 752 SerTyrSerSerValIleLeu 758  
 2297 CCGTACTCTGCTATCCTTCTT 2317  
 RESULT 8  
 US-09-198-452A-1  
 ; Sequence 1, Application US/09198452A  
 ; Patent No. 6559294  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Griffiths, R.  
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
 ; thereof and uses thereof, in particular for the diagnosis, prevention  
 ; TITLE OF INVENTION: and treatment of infection  
 ; FILE REFERENCE: 9710-003-999  
 ; CURRENT APPLICATION NUMBER: US/09/198,452A  
 ; CURRENT FILING DATE: 1998-11-24  
 ; NUMBER OF SEQ ID NOS: 6849  
 ; SEQ ID NO 1  
 ; LENGTH: 1230025  
 ; TYPE: DNA  
 ; ORGANISM: Chlamydia pneumoniae  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(15000)  
 ; OTHER INFORMATION: n=a or c or g or t  
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/	OTHER INFORMATION:	n=a or c or g or t
/	NAME/KEY:	misc feature
/	LOCATION:	(345001)..(360000)
/	OTHER INFORMATION:	n=a or c or g or t
/	NAME/KEY:	misc feature
/	LOCATION:	(360001)..(375000)
/	OTHER INFORMATION:	n=a or c or g or t
/	NAME/KEY:	misc feature
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/	OTHER INFORMATION:	n=a or c or g or t
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/	OTHER INFORMATION:	n=a or c or g or t
/	NAME/KEY:	misc feature
/	LOCATION:	(405001)..(420000)
/	OTHER INFORMATION:	n=a or c or g or t
/	NAME/KEY:	misc feature



OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (795001)..(810000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (810001)..(825000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (825001)..(840000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (840001)..(855000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (855001)..(870000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (870001)..(885000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (885001)..(900000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (900001)..(915000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature

## Alignment Scores:

Pred. No.: 1,75e-135 Length: 1230025  
 Score: 1305.50 Matches: 279  
 Percent Similarity: 56.03% Conservative: 88  
 Best Local Similarity: 42.60% Mismatches: 231  
 Query Match: 30.99% Indels: 57  
 DB: 4 Gaps: 16

US-09-674-817B-3 (1-764) x US-09-198-452A-1 (1-1230025)

Qy 61 MetProAlaProLeuGlyAlaThrAlaLeuAla---GlyGlyValAsnPheAlaValTyr 79  
 Db 445840 GTTCCTTTTACCTCTGCGGCTTCTAAATTTCCCAACCGCTATCGATTGCTTTATAT 445899  
 Qy 80 SerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAsp 99  
 Db 445900 GCTTCACAGCTACCGAGTCATCTTCTTTA-----ACAGAC 445938  
 Qy 100 ArgValThrGlu-----GluValProLeuAspProLeuMetAsnArgThrGlyAsnVal 117  
 Db 445939 GAAATTCAGAGTCATAGAGTCCCTTTTACCCGATACACACCGCGCGTGGAT 445998  
 Qy 118 TrpHisValPheLeuGlyGlyLeuHisAsnMetLeuTyrGlyTyrArgPheAspGly 137  
 Db 445999 TGGCATATAGAGATCGAGGTATTTCTGATCAATCGCTTATCGATTTCTGTTCTATGG 446058  
 Qy 138 ThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValValAspProTyr 157  
 Db 446059 CCT---AAAAAGCAT---GGAATGCAATACTCTTTTAAAGAAATATCTTCGAGATCCCTAT 446112  
 Qy 158 AlalysAlaValIleSerArgGlyGlyTyrGlyValProAlaArgGlyAsnAsn----- 175  
 Db 446113 GCGAAGAATATTCATCCCAAGAGTATTTGGTTCGGAAGAAACAGGGGGATATGCA 446172  
 Qy 176 ---CysTrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGlu 194  
 Db 446173 TTTTGTAT-----TTAAGGAACACCACTTTCTCTGGAT 446208  
 Qy 195 GlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArg 214  
 Db 446209 GGTGATCAGCTCTGCAATTTGCCCAAGAGAGATGATCATCTATGAGATGATGACGT 446268  
 Qy 215 GlyPheThrLysHisAspSerAsnValGluHisProGlyThrPheIleGlyAlaVal 234  
 Db 446269 TCCTTCACGCAATCTTCTTCTATAGGTTTCATGCTCCGGACCTTCTTAGGAATCAT 446328

Qy 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254  
 Db 446329 GAAAGATCGACCATCTGCATAAGCTGGAAATCAACGCTGTGAACCTTTACCTATCTTT 446388  
 Qy 255 GluPheAsnGluLeuGlyTyrSerThrSerSerSerLysMet-----AspPhe 270  
 Db 446389 GAGTTCGATGAGACTGCGCATCTTTTAGAAATTCGAAATTCCTTATCTGTGTGCAATAT 446448  
 Qy 271 TrpGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyLe 290  
 Db 446449 TGGGTTATGCTCCCTTAAATTTCTTCTCTGCGCAGCTATGCTTATGCTCTCT--- 446505  
 Qy 291 LysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLys 310  
 Db 446506 GATCCTTCGCTCCCAAGT-----AGAGAGTTTAAATTTAGTAAAGACCTTGCAACAA 446559  
 Qy 311 ArgGlyIleGluValIleLeuAspValPheAsnHisThrAlaGluGlyAsnGluAsn 330  
 Db 446560 GAAGTATTGAGGTCATCTTGTATGTTTGTITTAATCATCG-----GGCTTGCAA 446610  
 Qy 331 GlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLys 350  
 Db 446611 GGGACGACCTGCTCTTCTGCTTGGATAGACACTCCGAGCTATTATATTTAGATGCACAA 446670  
 Qy 351 GlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValVal 370  
 Db 446671 GGTCACTTTACAAATTTATTCAGGCTGTGGAACACTCTCAATACAAACCGCCGCCACG 446730  
 Qy 371 ArgGlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPhe 390  
 Db 446731 ACCCAATGATCTCGACATCTTACGTTATGGTAGAAGAAATGCATGCGATGGCTTC 446790  
 Qy 391 ArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrAspProValAsnVal 410  
 Db 446791 CGATTGATCTTGTCTGCTTCTTCTGCTGCTGCTCTCG----- 446829  
 Qy 411 TyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThrProPro 430  
 Db 446830 -----GGATCTCCCTTACATTCGCTCTCT 446853  
 Qy 431 LeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAla 450  
 Db 446854 GTTTTAGAGGCGATTTCTTTTGTATCTTACTTCGAGCACAAGATTTAGCTGAGCCT 446913  
 Qy 451 TrpAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTyrAsnVal---TrpSer 469  
 Db 446914 TGGGATGCTGCGGTTGTATCAGTGGGCTATTTCCCACTGCTCTCCAGATGGAGT 446973  
 Qy 470 GluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPhe 489  
 Db 446974 GAATGGAACGTCCTGATCGTGATACGTGAAGCAATTTCTTAATGGGATCAAAATCTC 447033  
 Qy 490 AlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArg 509  
 Db 447034 ATAGAACCTTTGCTCTAGAAATTCAGGATCTCAAGACATCTATCTCCACGCG----- 447087  
 Qy 510 LysProTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeu 529  
 Db 447088 TCGCTACAAATTCGATTAATGTCAGTTGCCATGATGTTTACGTTATGTTGACACT 447147  
 Qy 530 ValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsn 549  
 Db 447148 GTGACTTATAACCAACAAATATAGGCTAACCGAGAGGATATTCGTACGCGCAGACAT 447207  
 Qy 550 HisAsnLeuSerTrpAsnCysGlyGluGluGlyGlyPheAlaArgLeuSerValLysArg 569  
 Db 447208 CGCAACTACACTACATTTCCGACCGAGAGGAAACAGAGACCTTCGCTTCCTGAA 447267  
 Qy 570 LeuArgLysArgGlnMetArgAsnPheValCysLeuMetValSerGlnGlyValPro 589  
 Db 447268 GTTCGTGAAGACAGTACGAAATTTTCTTACTTGTGTTGCTCGCAAGGCAATTCG 447327  
 Qy 590 MetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyrCys 609

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Db 447328 ATGATTCAATCAGGAGATGAGTATGCCCATACCCGCGAAGCAATAACAACCGTTGGCT 447387
QY 610 HisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluGlnTyrSerGluLeuHis 629
Db 447388 TTGGATTGGAATGCAATATCTTCTTTGGATCAGCTTACCGCAAGCCTACACATGATG 447447
QY 630 ArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAsp 649
Db 447448 CACTTTCTCTGTATCTCATTTGCGTTCGAAAAAATAATAAACACATTTTAAATCGAGGC 447507
QY 650 PheProThrAlaLysArgLeuGlnTyrHisGlyHisGlnProGlyLysProAspTyrSer 669
Db 447508 TTCTTTCCATAAGGAATAAGTGTGGTAGATGCTATGGGAAATCCCATGACATGCGCG 447567
QY 670 GluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrVal 689
Db 447568 CCTGGAAT--TTCATTAGCATTTAAATAAATCGCAAAA--GGCATGTATATGTT 447621
QY 690 AlaPheAsnThrSerHisLeuProAlaValAluLeuProGlu 704
Db 447622 GCATTTCCGTTGGAGCTCAAGCAACTTGGCACCCTTACCTAAA 447666

RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 3.3e-125 Length: 4403765
Score: 1225.00 Matches: 280
Percent Similarity: 51.41% Conservative: 85
Best Local Similarity: 39.44% Mismatches: 263
Query Match: 29.08% Indels: 82
DB: 3 Gaps: 19

US-09-674-817B-3 (1-764) x US-09-103-840A-2 (1-4403765)
QY 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyValAsnPhe 76
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QY 77 AlavalTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeu 96
Db 1771611 TCGTTGTTCCAGATCGCCGAGAGAGTGCAGCTATGCTG-----ATC 1771567
QY 97 LysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsn 116
Db 1771566 GACGAGGACGCGCTCGAGTCCGCGATCCCGCTTGACGAGGTG-----GACGGGTAC 1771516
QY 117 ValTyrHisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAsp 136
Db 1770457
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Db 1771515 GTCTGGCATGCCTATCTGCGGAACATCACCCCGCGCCAGCGCTACGGGTTTCGTGTGCAC 1771456
QY 137 GlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValValAspPro 156
Db 1771455 GGGCGGTTTCAGCCCGCGCGCCATCGGTGTGACCCAGCAAGCTGTGTCTCGACCGC 1771396
QY 157 TyrAlaLysAlaValIleSerArgGlyGluTyrGly----- 168
Db 1771395 TATGGAGTCTGTTCCACGCGCATTTCACTTCGGGCGAGCGCTGTATTCCTATGACGTC 1771336
QY 169 -----ValProAlaArgGlyAsnAsnCysTyrProGlnMetAla 181
Db 1771335 AAGCGCGTCGACCCGACAGCAGCACTCCCGCATGTGTCAGCTCGCTGGCCACACTATGACC 1771276
QY 182 GlyMetIleProLeuProTyrSerThrPheAspTyrGluGlyAspLeuProLeuArgTyr 201
Db 1771275 AGCGTCGTGATCAATCCGTTCT-----TTCGACTGGCATACGACCGGTGCGCGCGCAC 1771222
QY 202 ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLys---HisAsp 220
Db 1771221 CGGTACACGAGACGCGTAATCTACGAAGCGCATGTCAAAGGCATGACACAGACCATCC 1771162
QY 221 SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys-----LeuAsp 238
Db 1771161 AGTATCCCGCCGAACTCCGGCGCACCTACGCGCGCCTGGCGCCACCCCGGTGATCATCGAC 1771102
QY 239 TyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGlu 258
Db 1771101 CACCTCAACGAGCTCAACGTCACCCCGCTTGAGTTGATGCGGTGCACAGTTCCTACAC 1771042
QY 259 LeuGluTyrSerThrSerSerLysMetAsnPheThrGlyTyrSerThrIleAsnPhe 278
Db 1771041 GACTCCCGGCTGCTGGACCTCGGCTTGCAGAACTACTCGGTTTACACACCTTCGATTTC 1770982
QY 279 PheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIle 298
Db 1770981 TTCGCCCGCCACCATCAATACGCTCG-----ACCCGCGAAGCGCGC---AGCCGGTA 1770931
QY 299 AsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAsp 318
Db 1770930 GCGGAGTTCAAAACCATGTCGCGAGCTGCACGAAGCGGCATCGAGGTTCATCTCGAC 1770871
QY 319 ValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGly 338
Db 1770870 GTGCTCTACACACACCGCTGAAGGCAACCACTTGGTTCGACGATCAACTTCGCGGA 1770811
QY 339 ValAspAsnThrThrTyrTyrMetLeuAlaProLysGly---GluPheTyr---AsnTyr 356
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QY 357 SerGlyCysGlyAsnThrPheAsnHisProValValArgGlnPheIleValAsp 376
Db 1770750 ACCGGTACCGGCAACAGCCTCAATGCCCGCCACACACACCTGCGAGTGCATGATGAT 1770691
QY 377 CysLeuArgTyrTyrValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSer 396
Db 1770690 TCGCTGCGCTACTGGGTGATCGAAATGCACGTCGCGGTTCCGTTTCGACTGCGCGTCC 1770631
QY 397 IleMetThrArgGlySerSerLeuTyrAspProValAsnValTyrGlyAlaProIleGlu 416
Db 1770630 ACCTGGCGCGCGAGCTGCACGACGTCACCGGCTGCGGCATTC----- 1770586
QY 417 GlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSer 436
Db 1770585 -----TTCGATCTCGTGCAA 1770571
QY 437 AsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---Gly 455
Db 1770570 CAAGATCCGGTGGTCAGTCAGTCAAGTGTATCCCGAGCCATGGGATGTCGGCGAAGGT 1770511
QY 456 LeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyr 475
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; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 3,31e-125 Length: 4411529
Score: 1225.00 Matches: 280
Percent Similarity: 51.41% Conservative: 85
Best Local Similarity: 39.44% Mismatches: 263
Query Match: 29.08% Indels: 82
Dbs: 3 Gaps: 19

US-09-674-817B-3 (1-764) x US-09-103-840A-1 (1-4411529)

QY 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPhe 76
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QY 77 AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAspLeu 96
Db 1771485 TCGTGTCTCCGAGATCGCGGAGAGTTCGAGTATGCTCTG-----ATC 1771441

QY 97 LysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsn 116
Db 1771440 GACGAGGACGGCGTCGAGTCGCGGATCCGCTTCGACGAGGTG-----GACGGGTAC 1771390

QY 117 ValTrpHisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAsp 136
Db 1771389 GTCTGGCATGCTATCTCTCGGACATCACCCCGCGGCGCTACGGGTTCGTGTGCAC 1771330

QY 137 GlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAspPro 156
Db 1771329 GGGCGGTTGACCGCGGCGCGCATCGGTGTGACCCCGACAGCTGCTGCTGACCGG 1771270

QY 157 TyrAlaLysAlaValIleSerArgGlyGluTyrGly----- 168
Db 1771269 TATGGAAAGTGTCTCCACGGCGATTTTCACCTTCGGCGAGCGCTGTATTCTCTATGACGTC 1771210

QY 169 -----ValProAlaArgGlyAsnAsnCysTrpProGlnMetAla 181
Db 1771209 AACGCGCTGACCGCGACGACACTCCCGATGTGTGACTCGCTGGCGCCACACTATGACC 1771150

QY 182 GlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyr 201
Db 1771149 AGCGTCGTGATCAATCCGTTT-----TTCGACTGGGCATACGACCGGTGCGCGCAC 1771096

QY 202 ProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLys---HisAsp 220
Db 1771095 CGGTACACGAGACGGTAAATCTACGAGCGCATGTCAAGCGCATGTCAAGCGCATGACACAGACCCATCCC 1771036

QY 221 SerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys-----LeuAsp 238
Db 1771035 AGTATCCCGCGCGAATCCGCGGCGACCTACGCGCGCTGGCGCCACCGGTGATCATCGAC 1770976

QY 239 TyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGlu 258
Db 1770975 CACCTCAACGAGCTCAACGTCAACCGCGTTGAGTTGATGCGCGGTGACACCTTCCTACAC 1770916

QY 259 LeuGluTyrSerThrSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhe 278
Db 1770915 GACTCCCGGTGCTGGAGCTCGGCTTGGAAACTACTTGGGTGTACACCTTCGGATTC 1770856

QY 279 PheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIle 298
Db 1770855 TTGCGCGCGCGACCATCAATACCGCTCG-----ACCGCGAAGCGCGG---AGCGCGGTA 1770805

QY 299 AsnGluPheThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAsp 318
Db 1770804 GCCGAGTTTCAAAACCATGTGTCGAGCCTGCGCAGCCTGCGCAGCCTGAGTTCATCTCGAC 1770745

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## RESULT 10

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US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1

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QY 319 ValValPheAsnHisThrAlaGluGlyAsnGluSerPheLeuSerPheLeuGly 338
Db 1770744 GTCGCTTACCAACACACCGCTGAGGCAACACCTTGGGTCGACGATCACTTTCGGGA 1770685
QY 339 ValAspAsnThrThrTyrTyrMetLeuAlaProLysGly---GluPheTyr---AsnTyr 356
Db 1770684 ATCGACAAACCCGCTACTACCGACTGATGGACACGACTTGAGTTCTACAAGGACTTC 1770625
QY 357 SerGlyCysGlyAsnThrPheAsnHisProValValArgGlnPheLeuValAsp 376
Db 1770624 ACCGGTACCGGCAACAGCCTCAATGCCCGCCACCCACACACCCCTGCAGCTGATCATGGAT 1770565
QY 377 CysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheLeuAlaSer 396
Db 1770564 TCGCTGCGCTACTGGGATGATCGAATCGACGTGACGGGTCCGGTTCCGACCTGGGGTCC 1770505
QY 397 IleMetThrArgLysSerLeuTrpAspProValAsnValTyrGlyAlaProIleGlu 416
Db 1770504 ACGTGGCCCGGAGCTGACGAGCTGACCGGCTGTCGCAATTC----- 1770460
QY 417 GlyAspMetIleThrThrGlyThrProLeuValThrProLeuLeuAspMetIleSer 436
Db 1770459 -----TTCGATCTGGTGCA 1770445
QY 437 AsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---Gly 455
Db 1770444 CAAGATCCGCTGCTCAGTCAGGTCAGCTGATCGCGAGCCATGGGTGTCGCGAGGT 1770385
QY 456 LeuTyrGlnValGlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyr 475
Db 1770384 GGGTACAGGTTGGCACTTCCCA-----GGACTGTGGAGGAATGGAACGCAAGTAC 1770331
QY 476 ArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGlu 495
Db 1770330 CGGACACCTGTCGGGACTACTGGGAGGCGACCGCCACCTAGCGAATTCGGCTCC 1770271
QY 496 CysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIle 515
Db 1770270 CGGCTGACCGGGTCGTGGAGCTCTACGAAGCAACCGCGCGCCGACGTCGACGATC 1770211
QY 516 AsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLys 535
Db 1770210 AATTTGCTACCGCCACGACGGGTTCACTCAACGACTGCTCTCGTACACGCAAG 1770151
QY 536 TyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsn 555
Db 1770150 CACAACGAGGCCAATGGCGAGAACACCGCGACGCGGGAAGCTACACCGATCGTGGAC 1770091
QY 556 CysGlyGluGlyGlnPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMet 575
Db 1770090 TGGCGGTGTCAGAGGCCCCACCGCATGACCCCGACATCTTGGCGTGGCGTCCCGCCAGATG 1770031
QY 576 ArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAsp 595
Db 1770030 CGCAACATGTGGGCCACGCTTATGTTGTCAGCGAGGACGCGGATGATCCGCCACGCGAC 1769971
QY 596 GluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsn 615
Db 1769970 GAGATTGGGCGCACCAATAACGCAACAAACGCTCTACTGCCAGGACTCCGAATTATCT 1769911
QY 616 TyrPheArgTrpAspLysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMet 635
Db 1769910 TGGATGATTGGTCATTGGTGGCAAGATGCCGATCTCTAGCTTTCGACCGCAAGGCG 1769851
QY 636 ThrLysPheArgLysGlu-----CysGlnGlyLeuGly 646
Db 1769850 ACGACCTTGGCAAGAACCAACAGGTGTTTCGCGACGCGCGTCTTTGAGGGTGAACCG 1769791
QY 647 LeuGluAspPheProThrAlaLysArgLeuGlnTrp-----HisGlyHisGlnPro 663
Db 1769790 ATCCGAGTGGCGACGAAGTCCCGGATATCGCTGTTGACACCGAGCGGTCGGGATG 1769731
QY 664 GlyLysProAspTrpSerGluAsn---SerArgPheValAlaPheSerMetLysAspGlu 682
Db 1769730 ACGCACGAGGATTGGGCGAGAGGCTTCACAGGTGTTGGCGTGTGTTCCTCAACGGTGAA 1769671
QY 683 -----ArgGlnGlyGlu-----IleTyrValala 690
Db 1769670 GCCATTACCGCACCGAGCCCGTGGTGGAGCGAGTAGTCGAGGATTCATTCTCTGTGTC 1769611
QY 691 PheAsnThrSerHisLeuProAlaValValGluLeuPro---GluArgAlaGlyArgArg 709
Db 1769610 TTCAACGCCCATGACACGAGCGTGGAGTTCGTATCGCGCATGACGGCTATGCGGACGAG 1769551
QY 710 TrpGluProValValAspThrGlyLysPro 719
Db 1769550 TGGACCGGAGAGCTGGATACCAACGATCCC 1769521

RESULT 11:
US-09-129-075-3
; Sequence 3, Application US/09129075
; Patent No. 6087149
; GENERAL INFORMATION:
; APPLICANT: Teutsumi, No. 6087149siko
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Starch Conversion Process
; FILE REFERENCE: 5262.204-US
; CURRENT APPLICATION NUMBER: US/09/129,075
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: 0787/97
; EARLIER FILING DATE: 1997-07-02
; EARLIER APPLICATION NUMBER: 60/055,967
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: PCT/DK98/00304
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 2181
; ORGANISM: Rhodothermus marinus
US-09-129-075-3

Alignment Scores:
Pred. No.: 1,43e-126 Length: 2181
Score: 1187.00 Matches: 294
Percent Similarity: 50.26% Conservative: 86
Best Local Similarity: 38.89% Mismatches: 242
Query Match: 28.18% Indels: 134
DB: 3 Gaps: 30

US-09-674-817B-3 (1-764) x US-09-129-075-3 (1-2181)
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Db 40 GTCTGGCCCGCGCGCTTATCCGCTGGTGCCACCTGGGACGGGCTGGGGCTCAACTTT 99
QY 77 AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThr---ProGluAsp 95
Db 100 GCCCTCTACAGCCAGCAGCGCGAGCGGTGCAACTGGTGTCTCGACCCACCGCGCAT 159
QY 96 LeuLysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGly 115
Db 160 CCGCGCGCTTCGCCACGATCGAA-----GTGACCGAAGCAGCAGGC 201
QY 116 AsnValTrpHisValPheIleGluGlyLeuHisAsnMetLeuTyrGlyTyrArgPhe 135
Db 202 CCGATCTGGCATGTGTACCTCCCGCGCTGGTCCCGCCAGCTCTACGGCTATCGGTC 261
QY 136 AspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAsp 155
Db 262 TACGGACCTTACCGCGCGGAGGACCGCTTCAATCCGAACAAGGTGCTGCTCGAC 321
QY 156 ProTyrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsn 175
Db 156 ProTyrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsn 175
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Db 322 CCCTACGCGAAGCCATC-----GGCCGCGCCCTTCGC----- 354  
Qy 176 CysTrpProGlnMet-----AlaGlyMetIleProLeu 186  
Db 355 ---TGGACACAGCCTCTTCGTTTACAAAATCGGCGATCCGCGGGGATCTGCTGC 411  
Qy 187 -----ProTyrSer-----ThrPheAsp 192  
Db 412 TCCGAGAAGACAGCGCTCCGTACGCGCCGCTGGAGCCGCTCGTGGAGGCTGTTCGAG 471  
Qy 193 TrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHis 212  
Db 472 TGGGGGACACCGCCCGCCGCGATTCCTCGGAAGACACGATCATCTACGAACGGCAC 531  
Qy 213 LeuArgGlyPheThrLysHisAspSerSerAsnValIleHisPro----- 227  
Db 532 GTCAAGGGCATCAGAG-----CTGCATCCGGAAGTGGCGGAGCG 573  
Qy 228 -----GlyThrPheIleGlyAlaValSerLys-----LeuAspTyrLeuLysGluLeu 243  
Db 574 CTGCGGGGACGATCTCGGGGCTGAOCTCGACCGCGGTCTGGACACCTGAAGCAGCTG 633  
Qy 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThr 263  
Db 634 GCGCTACACGATCCAGCTCTCTCGGTCCAGCAAAAGTCACGATCGGCACCTGGTC 693  
Qy 264 SerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThr 283  
Db 694 GAGCGCGGCTGGCGCACTACTGGGCTACAAATCCGCTCTGTACTTTGCGCGGAGCCC 753  
Qy 284 ArgTyr---ThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLys 302  
Db 754 GAGTACCCACGACGCGCCGATC-----TCGCGCTGCGCGAGTTCAAG 798  
Qy 303 ThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsn 322  
Db 799 ATGATGTGCGGGCGCTGATGCTGCGCGCTTCAGGTGATCTCGACGCTGCTACAAAC 858  
Qy 323 HisThrAlaGluGlyAsnGluAsnGlyProIleSerPheLysGlyValAspAsnThr 342  
Db 859 CACACGGCGAAGCGCGCTGCTGGCGCCACCGCTGCTGCGGGGATCGACAAACCGC 918  
Qy 343 ThrTyrTyrMetLeuAlaProLysGlyGluPheTyr-----AsnTyrSerGlyCysGly 360  
Db 919 GCCTACTACAGCGCGATCCGACAAACCGCGCTTCTGTCGATTACAGCGGCACCGGC 978  
Qy 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380  
Db 979 AACACGCTGGACGTGGGCAACCCCTACGCTCATCATGACACAGCTTCGCTAC 1038  
Qy 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400  
Db 1039 TGGGTCACTGAATGCACTGACGCGCTTCGTTGACCTGCGCGCGCTGGCCCGC 1098  
Qy 401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420  
Db 1099 -----GAGCTGTACGACGTG-----GACATGCTC 1122  
Qy 421 ThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIle 440  
Db 1123 TCGACC-----TTTTTTCAGTCTCATTCAGCAGGACCCGGTG 1158  
Qy 441 LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---GlyLeuTyrGlnVal 459  
Db 1159 CTCACCGAGGTCAAGCTCATCGCGAACCCCTGGACGCTGGCGCGGGGGTATCAGGTG 1218  
Qy 460 GlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleVal 479  
Db 1219 GGACATTTTCCC---TGGCAG---TGGACCGAGTGGAAACGGCGCTATCTGTGACGCGCTG 1272  
Qy 480 ArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGly 499  
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Qy 500 SerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCys 519  
Db 1333 TCCAGCGATCTGTACGAACGCTAGCGGTCTGCTCGCTTCTGATCAACTTCGTCAAG 1392  
Qy 520 AlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuPro 539  
Db 1393 GCGCACACGCGCTTTCACCTCGGAAGACCTGTGTACGTACAGAAAGACACACGAGCG 1452  
Qy 540 AsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlu 559  
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Qy 580 ValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHis 599  
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Qy 620 Asp-----LysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThr 636  
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Db 1801 -----AACCGCGAAGCGCCCGCAGCAGTCTGGTGGCAGCTGAGGTGCGCCATCGCG 1854  
Qy 667 -----AspTrpSerGluAsnSerArgPheValAlaPheSerMet----- 679  
Db 1855 CACGAGGACTGACC---AACCGGAGCTGACGCGCTTCGAGCTGCTGCTGACGGGAC 1911  
Qy 680 -----LysAspGlu-----ArgGlnGlyGluIleTyrValAla 690  
Db 1912 GCCATTTCAGGGGACGCGACGACGACGCGACCGCTTCGCGACGACAGCTTCTGATTCTG 1971  
Qy 691 PheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly----- 707  
Db 1972 TCAACAACGCGACGCGAAGCGCTGCGTGGTGGCGGAGGTATGCTCCTGTGGCAAG 2031  
Qy 708 ---ArgArgTrpGluProVal-----ValAspThrGlyLysProAla 720  
Db 2032 CCGCACCACTGGAGGTGCTCCCGTGTTCACGCAATGTGGAGCCCCCAGCGTGGCGC 2091  
Qy 721 ProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIle 736  
Db 2092 CCGCGCGAGACGCTGCTG-----CTCCCGCGCGGTGCTGACGCTG 2133  
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US-09-346-237-12  
; Sequence 12, Application US/09346237A  
; Patent No. 6265197  
; GENERAL INFORMATION:  
; APPLICANT: Bisgard-Frantzen, Henrik  
; APPLICANT: Svendsen, Allan  
; TITLE OF INVENTION: Starch Debranching Enzymes  
; FILE REFERENCE: 5629.200-US  
; CURRENT APPLICATION NUMBER: US/09/346,237A  
; CURRENT FILING DATE: 1999-07-01  
; EARLIER APPLICATION NUMBER: PA 1998 00868  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: 60/094,353  
; EARLIER FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Rhodotermus marinus DSM 4252
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
; OTHER INFORMATION: IscAmylase
US-09-346-237-12
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## Alignment Scores:

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Pred. No.: 1,43e-126 Length: 2181
Score: 1187.00 Matches: 294
Percent Similarity: 50.26% Conservative: 86
Best Local Similarity: 38.89% Mismatches: 242
Query Match: 28.18% Indels: 134
DB: 3 Gaps: 30
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US-09-674-817B-3 (1-764) x US-09-346-237-12 (1-2181)

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QY 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyValAsnPhe 76
Db 40 GTCTGGGCCCGCGCCTTATCCCGTGGTGGTCCACCTGGAGCGGCTGGCGTCAACTTT 99
QY 77 AlaValTyrSerGlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThr---ProGluAsp 95
Db 100 GCCTCTACAGCCAGCGAGCGGCGTGAATGGTGTCTCGACCAACCGGAGCAT 159
QY 96 LeuYsAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGly 115
Db 160 CCCCGCGCTTCGCGCACGATCGAA-----GTGACCGAAGCGGACGACGC 201
QY 116 AsnValTrpHisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPhe 135
Db 202 CCGATCTGGATGTGATCTCCCGCGCTCGCTCCCGCGCAGCTCTACGGCTATCGCGTC 261
QY 136 AspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAsp 155
Db 262 TAGGACCTTACCGCGCGGAGGAGCCACCGCTTCAATCCGAACAAAGTGTGCTCGAC 321
QY 156 ProTyrAlaYsAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsn 175
Db 322 CCCTACCGAAGGCCATC-----GGCGGCGCCCTTGC----- 354
QY 176 CysTrpProGlnMet-----AlaGlyMetIleProLeu 186
Db 355 ---TGGCACGACAGCCTCTTCGGTTACAAATCGGCGATCCGCGGGATCTGTCTGTT 411
QY 187 -----ProTyrSer-----ThrPheAsp 192
Db 412 TCGAAGAGACAGCGCTCGTACCGCGCGCTGGAGCGCTGTGGAGGCGTGTTCGAG 471
QY 193 TrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHis 212
Db 472 TGGGGACACCGCGCGCGCGATTCCTCGGGAAGACACGATCATCTACGAACGCGAC 531
QY 213 LeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPro----- 227
Db 532 GTCAAGGGCATCAGAG-----CTGCATCCGGAAGTGGCGGAGCGG 573
QY 228 -----GlyThrPheIleGlyAlaValSerLys-----LeuAspTyrLeuLysGluLeu 243
Db 574 CTCGGGGGACGATCTGGGGCTGACCTCGAGCGCGTGTGTGAGCACCTGAAGCAGCTG 633
QY 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThr 263
Db 634 GGGCTACACAGATCAGTCTCTTCGGTGCACGCAAAAGTGCACGATCGGACCTGGTC 693
QY 264 SerSerSerLysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThr 283
Db 694 GAGCGGGCGTGGCGCAACTACTGGGGCTACAATCCGCTCTGCTACTTTCGCGCGGAGCC 753
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QY 303 ThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsn 322
Db 799 ATGATGTGTGGCGCGTGTGATGTGCGGCTTCGAGGTGATGTCGACGTGTCTACAAC 858
QY 323 HisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThr 342
Db 859 CACACGGGCGAAGCGCGCTGGGCCCCACGCTGTGTTCCGGGCGCATCGACAAACCCG 918
QY 343 ThrTyrTyrMetLeuAlaProLysGlyGluPheTyr-----AsnTyrSerGlyCysGly 360
Db 919 GCCTACTACAAGCGCGATCCGAACACCGCGCTTTCGTGTCGATTACACGGGACCGCGC 978
QY 361 AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr 380
Db 979 AACACGCTGGACGTGGGCAACCCCTACGTCATCCAGCTCATCATGACAGCCCTGGCTAC 1038
QY 381 TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg 400
Db 1039 TGGGTCACTGAAATGCAGTTCGACGCTTTCGTTTCGACCTGGCGCGCGCGTGGCGCGC 1098
QY 401 GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle 420
Db 1099 -----GAGCTGTACGACGTG-----GACATGTGTC 1122
QY 421 ThrThrGlyThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIle 440
Db 1123 TCGACC-----TTTTTTCAGGTCAATTCACGAGGACCCGGTG 1158
QY 441 LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGly---GlyLeuTyrGlnVal 459
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QY 460 GlyGlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleVal 479
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Db 1273 CGCGCTTCTGGCGGGCGGATCGGGGCTCAACGCTGAGTTTGCACCGCTTTCGCGGC 1332
QY 500 SerProHisLeuTyrGlnAlaGlyArgLysProTrpHisSerIleAsnPheValCys 519
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QY 520 AlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuPro 539
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QY 560 GlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePhe 579
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QY 580 ValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHis 599
Db 1573 AGCAGCTCTTCTCTCGCAGGGCTGCCCATGCTGTGGCGCGCGAGCTGTCGCGC 1632
QY 600 ThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrp 619
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QY 620 Asp-----LysLysGluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThr 636
Db 1693 CAGCTCGACAGCGCGCAGCAGCAGTTCTGGAG-----TTCTGTGCCCGCAGCATC 1743
QY 637 LysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeu 656
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 Db 1912 GCCATTACGGGACCGACGAGCGAGCAGCAGCCGTTTCGGGACACACGTTTCTGATTCTG 1971  
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 Db 1972 TTCACACACGCGCAGCGAGCGGTGCGGTGCTGGTCCGGAGGTATGCTCCTGTGGCAAG 2031  
 Qy 708 ---ArgArgTrpGluProVal-----ValAspThrGlyLysProAla 720  
 Db 2032 CCGCACCATCGGAGGTGCTCCGGTGTTCACACGCAATGTGGAGCCCGCCACGTCGCG 2091  
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RESULT 13

US-09-544-123-3  
 ; Sequence 3, Application US/09544123  
 ; Patent No. 6448049  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tsutsumi, No. 6448049iko  
 ; APPLICANT: Bisgaard-Frantzen, Henrik  
 ; APPLICANT: Svendsen, Allan  
 ; TITLE OF INVENTION: Starch Conversion Process  
 ; FILE REFERENCE: 5262.204-US  
 ; CURRENT APPLICATION NUMBER: US/09/544,123  
 ; CURRENT FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 09/129,075  
 ; PRIOR FILING DATE: 1998-08-04  
 ; PRIOR APPLICATION NUMBER: 0787/97  
 ; PRIOR FILING DATE: 1997-07-02  
 ; PRIOR APPLICATION NUMBER: 60/055,867  
 ; PRIOR FILING DATE: 1997-08-13  
 ; PRIOR APPLICATION NUMBER: PCT/DK98/00304  
 ; PRIOR FILING DATE: 1998-07-02  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2181  
 ; TYPE: DNA  
 ; ORGANISM: Rhodothermus marinus  
 ; US-09-544-123-3

Alignment Scores:  
 Pred. No.: 1,43e-126 Length: 2181  
 Score: 1187.00 Matches: 294  
 Percent Similarity: 50.26% Conservative: 86  
 Best Local Similarity: 38.89% Mismatches: 242  
 Query Match: 28.18% Indels: 134  
 Gaps: 30

US-09-674-817B-3 (1-764) x US-09-544-123-3 (1-2181)

Qy 57 ValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPhe 76  
 Db 40 GTCTGGCGCGCGCGCCCTATCCGCTGGGTGCCACCTGGGAGCGGCTGGGCGTCACTTT 99  
 Qy 77 AlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThr---ProGluAsp 95  
 Db 100 GCCCTCTACAGCAGCAGCGCGGCGGTGCAACTGGTGTCTGCTGACACCGCCGAGCAT 159

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QY 473 GlyLysTyrArgAspIleValArgGlnPheIleLeuGlyThrAspGlyPheAlaGlyGly 492
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QY 513 HisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAsnLeuValThrTyr 532
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QY 533 AsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeu 552
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QY 553 SerTrpAsnCysGlyGluGlnGlyPheAlaArgLeuSerValLysArgLeuArgLys 572
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QY 573 ArgGlnMetArgAsnPheValCysLeuMetValSerGlnGlyValProMetPheTyr 592
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QY 632 CysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPhePro 651
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QY 691 PheAsnThrSerHisLeuProAlaValValGluLeuProGlu---ArgAlaGlyArgArg 709
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QY 710 TrpGluProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAspLeu 729
Db 1070 TGTACCGAGTGGTGGACATATCTCAAGTACCAGATGATTTTGTATTGAGGAGTG 1129
QY 730 ProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrPro 749
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QY 750 MetLeuSerTyrSerSerValIleLeu 758
Db 1154 GTTGGCCGCTACTCTGCTATCTTCTT 1180
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Search completed: August 10, 2004, 06:46:21  
Job time : 6306 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 10, 2004, 03:42:31 ; Search time 1434 Seconds  
(without alignments)  
2612.273 Million cell updates/sec

Title: US-09-674-817B-3

Perfect score: 4212  
Sequence: 1 SGAPRLRRWRPNATAGKV.....SNLYPMLSYGVILVREDY 764

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Xgapop 10.0 , Xgapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match %

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFM=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=200000000 -USER=US09674817 @cgn 1.1 553 @runat 04082004.155845.24587  
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=10 -XGAP=10 -XGAPEXT=0.5  
-Fgapop=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEX=7

Database : Published Applications NA:

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3:	/cgn2_6/ptodata/2/pubnpa/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubnpa/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/2/pubnpa/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/2/pubnpa/PCTUS_PUBCOMB.seq:
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19:	/cgn2_6/ptodata/2/pubnpa/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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	1	4148	98.5	2437	15	US-10-338-091-6	Sequence 6, Appli
	2	4050	96.2	2397	15	US-10-338-091-1	Sequence 1, Appli
	3	4050	96.2	2397	15	US-10-338-091-2	Sequence 2, Appli
	4	3597	85.4	2307	17	US-10-437-963-88689	Sequence 88689, A
	5	3569.5	84.7	2684	13	US-10-425-114-24609	Sequence 24609, A
	6	2895.5	68.7	2352	9	US-09-938-842A-218	Sequence 218, App
	7	2895.5	68.7	2352	11	US-09-938-842A-218	Sequence 218, App
	8	2895.5	68.7	2352	11	US-09-938-842A-218	Sequence 218, App
	9	2895.5	68.7	2352	11	US-09-938-842A-218	Sequence 218, App
	10	2153.5	51.1	1830	13	US-10-425-114-19788	Sequence 1, Appli
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	12	1638.5	38.9	2124	16	US-10-424-599-11817	Sequence 6193, Ap
	13	1553.5	36.9	2729	17	US-10-369-493-26385	Sequence 11817, A
	14	1526.5	36.2	2198	13	US-10-437-963-39232	Sequence 39232, A
	15	1368	33.0	2241	16	US-10-425-114-20367	Sequence 39232, A
	16	1305.5	31.0	1995	9	US-10-369-493-26296	Sequence 26296, A
	17	1305.5	31.0	1995	9	US-10-369-493-26296	Sequence 26296, A
	18	1305.5	31.0	1995	9	US-10-369-493-26296	Sequence 26296, A
	19	1300	30.9	1998	13	US-09-841-132-381	Sequence 381, App
	20	1294.5	30.7	2103	16	US-10-282-122A-18612	Sequence 18612, A
	21	1283.5	30.5	2106	16	US-10-282-122A-18612	Sequence 18612, A
	22	1268	30.1	2163	16	US-10-282-122A-18612	Sequence 18612, A
	23	1264	30.0	2001	13	US-10-369-493-42960	Sequence 42960, A
	24	1261	29.9	2039	16	US-10-369-493-42960	Sequence 42960, A
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	38	1187	28.2	2181	15	US-10-375-720-12	Sequence 12, Appli
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	40	1183.5	28.1	2226	16	US-10-369-493-28419	Sequence 28419, A
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	42	1164.5	27.6	2065	16	US-10-369-493-32052	Sequence 32052, A
	43	1162.5	27.6	2100	16	US-10-369-493-32052	Sequence 32052, A
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	45	1149.5	27.3	2151	15	US-10-369-493-32052	Sequence 32052, A

#### ALIGNMENTS

#### RESULT 1

US-10-238-091-6  
Sequence 6, Application US/10238091  
Publication No. US20030093834A1  
GENERAL INFORMATION:  
APPLICANT: Hoechst Schering AgrEvo GmbH  
APPLICANT: LIRZ, Horst  
APPLICANT: LSTTICKE, Stephanie  
APPLICANT: ABEL, Gernot  
APPLICANT: GENSCHER, Ulrich  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT  
FILE REFERENCE: 514413-3849.1  
CURRENT APPLICATION NUMBER: US/10/238,091  
CURRENT FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: WO 99/58690  
PRIOR FILING DATE: 1999-11-18  
PRIOR APPLICATION NUMBER: DE 198 20 608.9  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: 09/674,817  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1

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TYPE: DNA	Db	856	ACGACATACATCAGCGGSAATAAACTGTGGCGTATGCCATAAATGAGTTCAA	915
ORGANISM: Triticum aestivum L. cv. Florida	Qy	303	ThrPheValArgGluAlaHisLysArgGlyLeuValileLeuAspValValPheAsn	322
FEATURE:	Db	916	ACTTTTGAAGAGAGGCTCACAAACGGGGAATTTAGGATGCTGATGTTCTTCAC	975
NAME/KEY: CDS	Qy	323	HisThrAlaGluGlyAsnGluAsnGlyProileLysSerPheLysGlyValAspAsnThr	342
LOCATION: (16)...(2304)	Db	976	CATACAGCTGAGGGAATGAGAAATGTCCTCAATTTATCATTTAGGGGGTTCGATAATCT	1035
OTHER INFORMATION:	Qy	343	ThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThr	362
US-10-238-091-6	Db	1036	ACATACATATATGCTTGCAACCCAGGGAGATTTATAACTATTTCTGGCTGGGAATACC	1095
Alignment Scores:	Qy	363	PheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTrpVal	382
Pred. No.: 0	Db	1096	TTCAACTGTATATCATCTGCTGCTGCTCAATTTGATGATTTGTTTAAAGATACTGGGTG	1155
Score: 4148.00	Qy	383	ThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySer	402
Matches: 750	Db	1156	ACGGAAATGCATGTTGATGTTTTCGTTTTCATCTTCATCCATTAATGACAGAGTTCC	1215
Percent Similarity: 99.08%	Qy	403	SerLeuTrpAspProValAsnValTyrGlyValAlaProileGluGlyAspMetIleThr	422
Best Local Similarity: 98.43%	Db	1216	AGTCTGTGGATCCAGTTAAACGTGTATGGAGCTCCAAATGAAGGTGACATGATCAACA	1275
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Query Match: 98.48%	Db	1276	GGGACACTCTTGTACTCCACCACTTATGACATGATCAGCAATGACCAATCTTGA	1335
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Gaps: 15	Db	1336	GGCGTCAAGCTCGTTGTAAGCATGGATGTCAGGAGGCTCTATCAAGTAGGTCAATTC	1395
US-09-674-817B-3 (1-764) x US-10-238-091-6 (1-2437)	Qy	463	ProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPhe	482
3 ProAlaProArgLeuArgTrpArgProAsnAlaThrAlaGlyLysGlyValGlyGlu	Db	1396	CTCCTCAGTGAATGTTTGTCTGAGTGGATGGAGATACCGGACATCTTGGTCAATTC	1455
16 CGGCGCCGCGCTCGACGCGTGGCGGCCCAATGCGACGCGCGGGAAGGGGTTCGGCGAG	Qy	483	IleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHis	502
23 ValCysAlaAlaValValGluAlaThrLysValGluAspGluGlyGluLysGlu	Db	1456	ATTAAGGCACTGATGATTTGCTGGTGGTTTTCGCGAATGTCTTGTGGAAGTCCACAC	1515
76 GTCGCGCGCGGTGTGAGTGGCGACGAAGCGGAGATGAGGGGAGGAGGAGCGAG	Qy	503	LeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisAsp	522
43 ProValAlaGluAspArgTyrAlaLeuGlyAlaCysArgValLeuAlaGlyMetPro	Db	1516	CTATACCAAGCAGGAGGAGAGAAACCTTGCCACAGTATCAACTTGTATGTGCACACGAT	1575
136 CGGTCGCGGAGACAGGTACGCGCTCGCGCGCGCTCGACGGTCTCGCGGAATGCC	Qy	523	GlyPheThrLeuAlaAspLeuValThrTyrAsnLysIleTyrAsnLeuProAsnGlyGlu	542
63 AlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGlyGly	Db	1576	GGATTTACACTGCTGATTTGGTAACATATAATAACAAAGTACAAATTTACCAATGGGAG	1635
196 AGCGCTCGGCGCCACCGCTCGCGCGCGGGGTCATTTTCGCGCTACTCCCGCGGA	Qy	543	AsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnGlyGluGlyGluPhe	562
83 AlaThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgValThr	Db	1636	AACAACAGAGATGAGGAAATCAACATCTTGTGCTGAAATTTGGGAGGAGGAGNAATTC	1695
256 GCCACAGCGCGCGCTCTGCTCTTCACGCGCAGAAAGATCTCAAGGCGGATAGGTCACG	Qy	563	AlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeu	582
103 GluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIle	Db	1696	GCAAGATTTGCTGTCAAAAGATTTGAGGAGAGGAGCAGATGCGCAATTTCTTTGTCTCTC	1755
316 GAGGAGTTCCCTTACCCCTGATGAATCGACGCGGAGATGATGCTTAAAGGAGTATC	Qy	593	MetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGly	602
123 GluGlyGluLeuHisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHis	Db	1756	ATGGTTTCTCAGAGATTTCCAAATGTTCTACNTGGGTGATGAATATGCCACACAAAGGG	1815
376 GAAGGCGAGCTGCAGGACATGCTTTACGGGTACAGGTTCGACGCGCACCTTTGCTCTC	Qy	603	GlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLys	622
143 CysGlyHisTyrLeuAspValSerAsnValValValAspProTyrAlaLysAlaValle	Db	1816	GGCAACCAACATACATACTGCTGCTGCTTATGTCAATTTATTTTGGTGGGATAAAAA	1875
436 TCGGGCACTACTCTGATGTTTCCAAATGCTGGTGGATCTTATGCTTAAAGGAGTATA	Qy	623	GluGlnTyrSerGluLeuHisArgPheCysLeuMetThrLysPheArgLysGluCys	642
163 SerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGly	Db			
496 AGCGGAGGAGATGATGGTGTTCGCGCGCGTGGTAACAAATTCGCTGCGCTCAGATGGCTGC	Qy			
183 MetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrPro	Db			
556 ATGATCCCTCTTCATATAGACGTTTGAATGGGAGGCGACCTACCTCTAAGATATCCT	Qy			
203 GlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSer	Db			
616 CAAAGGACCTGTAATATAGATGACATGCTGCGTGGATTCACGAAGCATGATTCACGC	Qy			
223 AsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGlu	Db			
676 AATGTAGAACATCCCGTACTTTCATCTGGGCTGTGTCGAAGCTTGACTATTTCAAGGAG	Qy			
243 LeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSer	Db			
736 CTGGAGTTAAATTGATTGAGTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	Qy			
263 ThrSerSerLysMetAsnPheThrGlyTyrSerThrIleAsnPhePheSerProMet	Db			

Db 1876 GAACAATACTCTGACTTGACCGATTCTGTGCTCATGACCAAAATTCGCAAGGAGTGC 1935  
Qy 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662  
Db 1936 GAGGGTCTTGGGCTTGAGGATTTTCCACAGCGCGGAACGGCTCGAGTGGCATGTCATCAG 1995  
Qy 663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682  
Db 1996 CCGTGGAGCGCTGATTGGTCTGAGATAGCCGATTCTGCTTTTCCATGAAGATGAA 2055  
Qy 683 ArgGlnGlyGluLeuTrpValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702  
Db 2056 ACACAGGGCGAGATCTATGTGCTTCAACACAGCCACTTACCGCGCTTGTTCAGTCTC 2115  
Qy 703 ProGluArgAlaGlyArgTrpGluProValValAspThrGlyLysProAlaProTyr 722  
Db 2116 CCGAGCGCACAGGGCGCGTGGNACCGGTGGTGGACAGGCAAGCCAGCACCATAC 2175  
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742  
Db 2176 GACTTCCTCACTGACGACTTACCTGATCGCGCTCTCACCATACACGAGTTCTCTCATTT 2235  
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762  
Db 2236 CTCACCTCCAACTCTTACCCCATGCTCAGCTACTCATCGTCTCATCTAGTATGCGCCT 2295  
Qy 763 AspVal 764  
Db 2296 GATGTT 2301

## RESULT 2

US-10-238-091-1  
; Sequence 1, Application US/10238091  
; Publication No. US20030093834A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoechst Schering AgrEvo GmbH  
; APPLICANT: LTRZ, Horst  
; APPLICANT: LSTICKS, Stephanie  
; APPLICANT: ABEL, Gernot  
; APPLICANT: GENSCHER, Ulrich  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT  
; FILE REFERENCE: 514413-3849.1  
; CURRENT APPLICATION NUMBER: US/10/238,091  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: WO 99/58690  
; PRIOR FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: DE 198 20 608.9  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: 09/574,817  
; PRIOR FILING DATE: 2000-11-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2997  
; TYPE: DNA  
; ORGANISM: Triticum aestivum L. cv. Florida  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(296)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (397)..(1617)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2145)..(2960)  
; OTHER INFORMATION:  
US-10-238-091-1

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Pred. No.: 0 Length: 2997

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Percent Similarity: 78.34% Conservative: 0  
Best Local Similarity: 78.34% Mismatches: 1  
Query Match: 96.15% Indels: 211  
DB: 15 Gaps: 2  
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Db 3 TCGGGGCGCGCGCGCGCTCGACGCGTGGCGACCCCAATCGACGGCGGGAAGGGGCTC 62  
Qy 21 GlyGluValCysAlaAlaValValGluAlaThrLysValGluAspGluGlyGluGlu 40  
Db 53 GCGAGGTGTGCGCGCGGTTCGTAGCGCGCGACGAGGTAGAGACGAGGGGAGAG 122  
Qy 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyAlaCysArgValLeuAlaGly 60  
Db 123 GACGAGCGGTGGCGGAGGACAGGTACGCGCTCGCGCGCGCTCGACGGTCTCGCGGA 182  
Qy 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyValValAsnPheAlaValTyrSer 80  
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Qy 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97  
Db 243 GCGGAGCCACCGCGCGCGCTCTGCTCTTCAGGCCAGAGATCTCAAGGCGGTGGG 302  
Qy 97 ----- 97  
Db 303 TTGCCTCCGAGTAGAGTTTCATCAGCTTTCGCGCGCGCGCTTTTGGGCGCTG 362  
Qy 98 -----Ala-AspArgValThrGluGluValProLe 107  
Db 363 CAATTAAAGTTTGTACTGGGCAATGCTGCAGATAGGCTGACCGAGAGGTTCCCT 422  
Qy 107 uAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyLeuHi 127  
Db 423 TGACCCCTGATGAATCGGACCGGACAGTGTGCATGTCTTCATCGAAGCGAGTGA 482  
Qy 127 sAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLe 147  
Db 483 CAATGCTTTACGGGTACAGGTTCGACGCGACCTTTGCTCTCTCCTGCGGCGACTACCT 542  
Qy 147 uAspValSerAsnValValValAspProTyrAlaLysAlaValIleSerArgGlyGluTy 167  
Db 543 TGATGTTTCCAATGCTCGTGTGATCCTTATGTAAGCAGTGATTAAGCCGAGGAGTA 602  
Qy 167 xGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuPr 187  
Db 603 TGGTGTTCACGCGCTGGTAACAAATTGCTGCGCTCAGATGGCTGGCATGCTCTCTTCC 662  
Qy 187 cTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuVa 207  
Db 563 ATATAGCACGTTTGATGGAGCGCGACCTACCTCTAAGATATCTCAAGAGACCTGGT 722  
Qy 207 lIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr 227  
Db 723 AATATATGAGATGCACTTGGTGGATTTCAGAGCATGATTCAAGCAATTCAGAACATCC 782  
Qy 227 oGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCy 247  
Db 783 GGGTACTTTTCATTTGGAGCTGTGTCGAGCTTGACTTATTTGAAGAGAGCTTGGAGTTAATTG 842  
Qy 247 sIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSerLy 267  
Db 843 TATTGAATTAAATGCCCTGCCATGAGTTCAACGAGCTGGAGTACTCAACCTCTCTTCCAA 902  
Qy 267 sMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrse 287  
Db 903 GATGAACCTTTTGGGATATTCTACCAATAAATCTCTTTTCCCAATACAGATACATC 962  
Qy 287 rGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGl 307





; PRIOR APPLICATION NUMBER: WO 99/58690  
 ; PRIOR FILING DATE: 1999-11-18  
 ; PRIOR APPLICATION NUMBER: DE 198 20 608.9  
 ; PRIOR FILING DATE: 1998-05-08  
 ; PRIOR APPLICATION NUMBER: 09/674,817  
 ; PRIOR FILING DATE: 2000-11-06  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 2997  
 ; TYPE: DNA  
 ; ORGANISM: Triticum aestivum L. cvFlorida  
 US-10-238-091-2

## Alignment Scores:

Pred. No.: 0 Length: 2997  
 Score: 4050.00 Matches: 763  
 Percent Similarity: 78.34% Conservative: 0  
 Best Local Similarity: 78.34% Mismatches: 1  
 Query Match: 96.15% Indels: 211  
 DB: 15 Gaps: 2

US-09-674-817B-3 (1-764) x US-10-238-091-2 (1-2997)

QY 1 SerGlyProAlaProArgLeuArgArgTyrArgProAsnAlaThrAlaGlyLysGlyVal 20  
 Db 3 TCGGGCCGCGCGCGCGCTGGAGCGTGGCGACCCCAATGCCGACGCGCGGGAGGGGTC 62  
 QY 21 GlyGluValCysAlaAlaValGluAlaAlaThrLysValGluAspGluGlu 40  
 Db 63 GCGAGGTGGCGCGCGCTGTCGAGCGCGCGCGAGGAGTAGAGGACGAGGGGAGGAG 122  
 QY 41 AspGluProValAlaGluAspArgTyrAlaLeuGlyGlyValaCysArgValLeuAlaGly 60  
 Db 123 GACGACCGGTGGCGAGGACAGGTACGCGCTCGCGCGCGCGTGGCGGTGCTCCCGGA 182  
 QY 61 MetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyrSer 80  
 Db 183 ATGCCCGCGCGCTGGCGCGCACCGCGCTCGCGCGCGCGGTCAAATTCGCCGCTATTCC 242  
 QY 81 GlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAspLeuLys----- 97  
 Db 243 GCGGAGACCCCGCGCGCGCTGCTGCTCTTCACGCCAGAGACTCAAGCGCGTGGG 302  
 QY 97 ----- 97  
 Db 303 TTGCTCCCGAGTAGAGTTTCATCAGCTTTGCGTGGCGCGCGCCCTTTTGGGCGCTG 362  
 QY 98 -----Ala-AspArgValThrGluGluValProle 107  
 Db 363 CAATTTAAGTTTGTACTGGGGCAATGCTGCAGGATAGGGTGCACCGAGGAGTTCCCT 422  
 QY 107 uAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyGluLeuHi 127  
 Db 423 TGACCCCTGATGAATCGACCGGACGCTGTGGCATGCTTCATCGAAGGCGAGCTGCA 482  
 QY 127 sAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrIle 147  
 Db 483 CAACATGCTTACGGGTACAGGTTCGACGCGACCTTTGCTCTCACTGGCGGCACTACT 542  
 QY 147 uAspValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGluTy 167  
 Db 543 TGAATTTCAATGCTGGTGGATCCTTATGCTAAGGCGAGTGAAGCGGGGAGTA 602  
 QY 167 rGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuPr 187  
 Db 603 TGTGTTCACGCGGTGTAACAATGCTGGCTCAGATGGCTGGCATGATCCCTCTTCC 662  
 QY 187 oTyrSerThrPheAspTyrGluCysLeuProLeuArgTyrProGlnLysAspLeuVa 207  
 Db 663 ATATAGCAGGTTGATTTGGGAAGGGGACCTACTCTTAAGATATCTCAAAAGGACCTGGT 722  
 QY 207 lIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisPr 227

Db 723 AATATATGAGATGCACCTTGGTGGATTACAGACATGATTCAAGCAATGTAGAACATCC 782  
 QY 227 cGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCy 247  
 Db 783 GGGTACITTCATTGGAGCTGTGTCGAAGCTTGACTATTGAAGGAGCTTGGAGTAATTG 842  
 QY 247 sIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerLy 267  
 Db 843 TATTGAATTATGCCCTGCCATGAGTTCAACGAGCTGAGTACTCAACCTCTTCTTCCAA 902  
 QY 267 sMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSe 287  
 Db 903 GATGAACITTTGGGGATATCTACCATAAACTCTTTTCCCAATGACAGATACACATC 962  
 QY 287 rGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgG 307  
 Db 963 AGCGGGATAAAAAAGCTGGCGGTGATGCCATAAATGAGTTCAAAACTTTTGTAGAGA 1022  
 QY 307 uAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluG 327  
 Db 1023 GGCTCAAAACCGGGAAATGAGGTGATCCTGGATGTTGTTCTTCAACCATCAGCTGAGG 1082  
 QY 327 yAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLe 347  
 Db 1083 TAATGAGAAATGGTCCAATATTTATCATTTAAGGGGTGCGATAATACTACATATATGCT 1142  
 QY 347 uAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHi 367  
 Db 1143 TGCACCAAGGAGAGATTTATATACTATTCTGGCTGGGAATACCTTCAACTGTAATCA 1202  
 QY 367 sProValValArgGlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisVa 387  
 Db 1203 TCCTGTGGTTCGTCAATTCATTGTAGATTGTTTAAGATATCTGGTGACGGAAATGCAATG 1262  
 QY 387 lAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspPr 407  
 Db 1263 TGATGGTTTCGTTTGTATCTTGCATCCATAATGACAGAGGTTCCAGTCTGTGGGATCC 1322  
 QY 407 oValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuVa 427  
 Db 1323 AGTTAAGGTATAGAGCTCCATAGAAGTGCATGATCACACAGGACACCTCTTGT 1382  
 QY 427 lThrProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValLysLeuIl 447  
 Db 1383 TACTCCACCACTTATTCACATGATCAGCAATGACCAATTTCTTGGAGCGCTCAAGCTCAT 1442  
 QY 447 eAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnVa 467  
 Db 1443 TGCTGAAGCATGGGATGCAGAGCGCTCTATCAAGTAGGTCAATTCCTCTCAGTGAATGT 1502  
 QY 467 lTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAs 487  
 Db 1503 TTGCTCTGAGTGGATGGGAAGTACCGGACATTTGCGTCAATTCATTAAAGGCACTGA 1562  
 QY 487 pGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAla-- 506  
 Db 1563 TGGATTTGCTGGTGGTTTTCGGAATGCTTTTGGGAAGTCCACACCTATACCAGGT-AA 1621  
 QY 506 ----- 506  
 Db 1622 GTTGTGCAATACTTGTAAATGAGTTGAGTGAATGTCACCTGGATTTTTTATATATACCA 1681  
 QY 506 ----- 506  
 Db 1682 CATGATGATACACATCTAAATATATATAACAATCATAGTGTATGCATATGCAATTTGGCTAAG 1741  
 QY 506 ----- 506  
 Db 1742 AAGTATTAGTATACACTAGTGTATATATAGTTTTAAACCCCACTTGCCAAATGAAG 1801  
 QY 506 ----- 506

Db 1802 GAACATAGGGCTTCTAGTATATCTTATTATTGTCGGTGAATAATCCACTGAAAAATT 1861  
QY 506 ----- 506  
Db 1862 CCAGCCATGTCATTTTTRAGGGGGGAGNAGAACTATATGATTTGCCCTTAAAGA 1921  
QY 506 ----- 506  
Db 1922 AGCCATCTCAGAATTCATAGTAAGTTGCTTTCTGTAAAGAAAGAAAGCACTTCATA 1981  
QY 506 ----- 506  
Db 1982 CTTTCTACCGTGCTAACTTAGCTGATGATATATTTGAAGAAGATGCCAAATTTAATT 2041  
QY 506 ----- 506  
Db 2042 TGTCCGATATTTGATCTGTTATTCACAAATTTCTATTGTTTCTAGAAATCAAAACC 2101  
QY 507 ----- GlyGlyArgLysP 511  
Db 2102 AGTAACCTTGTATGGCACTGCAACTTCTATTGATTAAATCAGGCGAGGAGGAAGAAACC 2161  
QY 511 oTTPHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTh 531  
Db 2162 TTGGCACAGTATCAACTTTGTATGTGCATGATGGATTACACTGGCTGATTTGGTAAAC 2221  
QY 531 rTyraAsnLysLysTyraAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAs 551  
Db 2222 ATATAATAAGAGTACAAATTTACCAATGGGAGAACCAACAGAGATGGAGAAATACAA 2281  
QY 551 nLeuSerTPAsnCysGlyGluGluGluPheAlaArgLeuSerValLysArgLeuAr 571  
Db 2282 TCTTAGCTGGAATTTGGGGAGAGAGGAATTCGCAAGATTGCTCTCAAAAGATTGAG 2341  
QY 571 gLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPh 591  
Db 2342 GAAGAGCGAGATGGCGCAATTTCTTTGTTGTTCTCATGGTTTCTCAAGGAGTTCCAATGTT 2401  
QY 591 eTyraMetGlyAspGlyTyraGlyHisThrLysGlyLysAsnAsnAsnThrTyraCysHisAs 611  
Db 2402 CTACATGGGTGATGAATATGGCCACACAAAGGGGGGCAACACAAATACATATCGCATGA 2461  
QY 611 pSerTyraValAsnTyraPheArgTPAspLysLysGluGlnTyraSerGluLeuHisArgPh 631  
Db 2462 TTCCTATGTCATTTATTTTCGTGGATPAAAGAAAGCAATATCTCTGAGTTGCACCGATT 2521  
QY 631 eCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPhePr 651  
Db 2522 CTGCTGCTCTCATGACCAAAATTCGCAAGGAGTGCAGAGGCTCTTGGCCTTGAGGACTTTCC 2581  
QY 651 oThrAlaLysArgLeuGlnTyraHisGlyHisGlnProGlyLysProAspTPSerGluAs 671  
Db 2582 AACGGCCAAACGGCTGCTGATGGTATCATCAGCTGGGAAGCTGATGGTCTGAGAA 2641  
QY 671 nSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyraValAlaPh 691  
Db 2642 TAGCCGATTCGTTGCTTTTCCATGAAGATGAAAGACAGGGCGAGATCTATGTGGCCTT 2701  
QY 691 eAsnThrSerHisLeuProAlaValGluLeuProGluArgAlaGlyArgArgTPG 711  
Db 2702 CAACACACGCCACTTACCGGGCGTGTGTAGCTCCAGAGCGCGAGGGCGCGGTGGGA 2761  
QY 711 uProValValAspThrGlyLysProAlaProTyraPheLeuThrAspAspLeuProAs 731  
Db 2762 ACCGGTGGTGACACAGGCAAGCCACCATACGACTTCTCTCACCGAGCTTACCTGA 2821  
QY 731 pArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyraSerAsnLeuTyraProMetLe 751  
Db 2822 TCGCGCTCTCACATACACAGTTCTCGCATTTCTCTACTCTCAACACCTCTACCCCATGCT 2881  
QY 751 uSerTyraSerValIleLeuValLeuArgProAspVal 764  
Db 2882 CAGCTACTCATCGGTCACTAGTATTGGCCCTCATGATT 2921

## RESULT 4

US-10-437-963-88689  
; Sequence 88689, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION: Thomas J.  
; APPLICANT: La Rosa, David K.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 88689  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MPT4530\_87515C.1  
US-10-437-963-88689  
Alignment Scores:  
Pred. No.: 0 Length: 2307  
Score: 3597.00 Matches: 644  
Percent Similarity: 92.98% Conservative: 31  
Best Local Similarity: 88.71% Mismatches: 45  
Query Match: 85.40% Indels: 6  
DB: 17 Gaps: 1  
US-09-674-817B-3 (1-764) x US-10-437-963-88689 (1-2307)

QY 44 ValAlaGluAspArgTyraAlaLeuGlyAlaCysArgValLeuAlaGlyMetProAla 63  
Db 13 GTGATCGGAGGAGGTACCGCTGGGTGGCGGTGCGGTGCTCCCGGAATGCCCGG 72  
QY 64 ProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsnPheAlaValTyraSerGlyGlyAla 93  
Db 73 CGGCTCGGGGCCACCGCTCGACGCGGGGTCAATTCCCGCTCTACTCCGCGCGGCA 132  
QY 84 ThrAlaAlaLeuCysLeuPheThrProGluAspLeuLysAlaAspArgValThrGlu 103  
Db 133 TCCGCGCGCGTCTGCTCTTTCACCCCGGAGATCTCGAGCGGATGAGGTGACTGAG 192  
QY 104 GluValProLeuAspProLeuMetAsnArgThrGlyAsnValTyraHisValPheIleGlu 123  
Db 193 GAGGTTCCGCTTGATCTCTGTTCAATCGGACGGGGAATGTGTGGCACGCTTCATCGAA 252  
QY 124 GlyGluLeuHisAsnMetLeuTyraGlyTyraArgPheAspGlyThrPheAlaProHisCys 143  
Db 253 GGGGAGCTGCACAAACATGCTGTACGGGTACAGGTTCCGATGGTATGTTCCCGCTCACTGC 312  
QY 144 GlyHisTyraLeuAspValSerAsnValValAspProTyraAlaLysAlaValIleSer 163  
Db 313 GGCAGTACTTCGATGTTCTCCAAATGTCGTGGTGGATCTTATGCCAAGGAGGTGATAAGC 372  
QY 164 ArgGlyGluTyraGlyValProAlaArgGlyAsnAsnCysTyraProGlnMetAlaGlyMet 183  
Db 373 CGAGGAGATGATGGTGTCCCGGCTCCCTGCTGGGGAATGTGTGGCCTCAATGGGTGCATG 432  
QY 184 IleProLeuProTyraSerThrPheAspTPGluGlyAspLeuProLeuArgTyraProGln 203  
Db 433 ATCCCTCTCCGTACAGTACGTTTGAATGGCAAGGTACCTACCTCTGAGATATCTCTAG 492  
QY 204 LysAspLeuValIleTyraGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsn 223  
Db 493 AAGGATCTTGTAAATCTATGAGATGCAATTTACGTGGGTTTACAAAGCACAGTTCAGCAAT 552

QY 224 ValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeu 243  
 DB 553 GTAGAACATCCAGGACTTACATTGGGCTATATCAAGCTTGACATATCTGAAGAGCTT 612  
 QY 244 GlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThr 263  
 DB 613 GGAGTTAACTGTGTAGAGTTGATGCGCTCCATGTAATCAATGAGCTGGAGTACTTCAGC 672  
 QY 264 SerSerSerLysMetAsnPheTyrGlyTyrSerThrIleAsnPhePheSerProMetThr 283  
 DB 673 TGTCTCTCCAGATGAACCTTCGGGATACTCCAGATAACTTTTTCACCAATGATA 732  
 QY 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303  
 DB 733 AGATATTTCATCAGTGGGATAGAAACTGTGGCGGTGATGCCATAAATGAATCAAAACT 792  
 QY 304 PheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValPheAsnHis 323  
 DB 793 TTGTGTAGAGGCTCACAAACGGGAATGAGTGATCATGATGTTGTCTTCAATCAT 852  
 QY 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343  
 DB 853 ACAGCCGAGGTAATGAGAAAGGACCAATATTATCATTTAGGGGATAGATAAATAGCACA 912  
 QY 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363  
 DB 913 TACTATATGCTGCCCTCAAGGAGAGATTTTACAATATTCCTGTTGTGGGAATACCTTC 972  
 QY 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTyrValThr 383  
 DB 973 AACTGTAAATCATCTCTGTCGTCGATTTATTTAGATGTTTAAAGATAGTGGTGACA 1032  
 QY 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403  
 DB 1033 GAAATGCATGTTGATGGTTTTCGTTTGTATCTTGCATCCATTAATGACCAGAGGATGCAGT 1092  
 QY 404 LeuTyrAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGly 423  
 DB 1093 CTTTGGGATCCAGTTAATGTATGAGAGTCCAGTAGAAGGTGACATGACTACGACAGGG 1152  
 QY 424 ThrProLeuValThrProProLeuLeuAspMetIleSerAsnAspProIleLeuGlyGly 443  
 DB 1153 ACACCTCTTGTCTACTCCACCCTATTGACATGATCAGCAATGATCCAAATCTTCGAGAT 1212  
 QY 444 ValLysLeuIleAlaGluAlaThrAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463  
 DB 1213 GTCAAGCTCATGCTGAAGCATGGAGTCGGAGGCGCTCTATCAAGTAGTCAATTTCT 1272  
 QY 464 HisTrpAsnValTrpSerGluTrpAsn-----GlyLysTyrArgAsp 477  
 DB 1273 CACTGGAATAATTGGTCAGATGGAATGGAAGGGCATGGGTATGGAAGTACCGGAC 1332  
 QY 478 IleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeu 497  
 DB 1333 ATTGTTTCGTCATTCATTAAAGGCACAGATGGATTGCTGTGTGTTTCGCTGAAATGTTG 1392  
 QY 498 CysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPhe 517  
 DB 1393 TGTGGAGTCCACATCTATCCAGCGAGGGGGAGGAACCTTGGCAGATCAACTTT 1452  
 QY 518 ValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsn 537  
 DB 1453 GTGTGTGCGCATGATGGAATTTACGCTGCTGATTTGGTGACATATAACAAGAAGTACAAC 1512  
 QY 538 LeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGly 557  
 DB 1513 TCTTCAAAATGGTGAGGATTAATAGATGGAGAAATCATAACTCAGCTGGAACTGTGGG 1572  
 QY 558 GluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsn 577  
 DB 1573 GAGGAAGGAGAAATTCACGTTTTCGTCGTCANAAAGATTGAGGAAGGCAATGCGCAT 1632

QY 578 PhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyr 597  
 DB 1633 TTCTTTGTTTCTCTCATGGTTTCTCAAGGTGTTCCGATGTTCTACATGGGCGATGAATAT 1692  
 QY 598 GlyHisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPhe 617  
 DB 1693 GGCCATACAAAGAGGACCAACAACACATCTACTGCCCATGACCAATTAATGTCATATTTC 1752  
 QY 618 ArgTrpAspLysLysGluLeuTyrSerGluLeuHisArgPheCysCysLeuMetThrLys 637  
 DB 1753 CGCTGGGACAAAGAAGAAATCCTCTGACTTGCACACGGTTCCTCTCTTATGACCAAA 1812  
 QY 638 PheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGln 657  
 DB 1813 TTCCGCCAAACAATCGGAGTCCCTTGGCTCGCAGACTTCCCAACAGCTCAACGGTTGCAT 1872  
 QY 658 TrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPhe 677  
 DB 1873 TGGCATGCCATACAGCTTGGAAACCTGACTGGTCTGAGACAAGCCGTTTCGTGGCCTTC 1932  
 QY 678 SerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuPro 697  
 DB 1933 TCCACGAAGATGAACGAAGAGCGAGATCTACGTGGCTTCAACGCCAGCAATTTGCCG 1992  
 QY 698 AlaValValGluLeuProGluArgAlaGlyArgArgTrpGluProValValAsnThrGly 717  
 DB 1993 GCGTTGTGGACTCCAGAGCGCCAGGCTACCGCTGGAGCGGCTGGTGACACAGGC 2052  
 QY 718 LysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHis 737  
 DB 2053 AAGCAGCGCTTATGACTTCTCCAGCAGACCTGCTGATCGTGTCTACGCGGTCCAC 2112  
 QY 738 GlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIle 757  
 DB 2113 CTGTTCTCTCATTTCCCAACTCCAATCTACCCCATGCTCAGCTACTCCTCATCATC 2172  
 QY 758 LeuValLeuArgProAsp 763  
 DB 2173 CTTGAATTGACGCTGAT 2190

## RESULT 5

US-10-425-114-24609  
 ; Sequence 24609, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53)131B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 24609  
 ; LENGTH: 2684  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3632-046-B8\_FLI  
 US-10-425-114-24609

Alignment Scores:  
 Pred. No.: 0 Length: 2684  
 Score: 3569.50 Matches: 653  
 Percent Similarity: 90.28% Conservative: 44  
 Best Local Similarity: 84.59% Mismatches: 65  
 Query Match: 84.75% Indels: 10  
 DB: 13 Gaps: 4

US-09-674-817B-3 (1-764) x US-10-425-1114-24609 (1-2684)

QY 2 GlyProAlaProArgLeuArg-ArgTrrArgProAsnAlaThrAlaGlyLysGlyValGl 21  
Db 175 GGGCGGTCGGCGCGGGTGGCGGGCGGCCCAAT---GTGGCGGACTGGGGCGGGG 231  
QY 21 yGluVal-----CysAlaAlaValValGluAlaAlaThrLysValGl 35  
Db 232 GCGGTCGTCTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGGA 291  
QY 35 uAspGluGlyGluGluAspGluProValAlaGluAspArgTrrAlaLeuGlyGlyAlaCy 55  
Db 292 GGACGCGACGACGACGACGACGAGGTGGCCGAGGAGGTTCGGCGTGGCGCGCGCGT 351  
QY 55 sArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAs 75  
Db 352 CCGGTCGTTCGGGAAATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTCAA 411  
QY 75 nPheAlaValTyrSerGlyGlyAlaThrAlaAlaAlaLeuCysLeuPheThrProGluAs 95  
Db 412 CTTGCGCGTCTACTCCAGCGGTCCCTCCCGCGGTCCGCTGCTTCGCTCCCGCGGA 471  
QY 95 pLeuLysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnA-gThrGl 115  
Db 472 CTTCAAGCGGATAGGTGACCGAGAGGTGCCCTCGATCCCTGCTCAACCGAACGGG 531  
QY 115 yAsnValTrrHisValPheIleGluGly---GluLeuHisAsnMetLeuTyrGlyTyrAr 134  
Db 532 AAACGTCGTGGCAGTTCATCCAGCGGACAGCTGCACCGCATGCTCTACGGATACAG 591  
QY 134 gPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValVa 154  
Db 592 GTTCGATGGCGTTCGCCCTTCAGCGCGACAGTACTACGATGTCCACAGTGTGCT 651  
QY 154 lAspProTrrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAs 174  
Db 652 GGATCCATACGTCATAGCGAGTGTAGCGAGGTGAATATGTTGTCCTCGCGCTGGTGG 711  
QY 174 nAsnCysTrrProGlnMetAlaGlyMetIleProLeuProTrrSerThrPheAspTrrGl 194  
Db 712 TAGTTTGGCCCTCAATGGCTGGTATGATGATCCCTCTCCCTATAAATGTTGATGGCA 771  
QY 194 uGlyAspLeuProLeuArgTrrProGlnLysAspLeuValIleTyrGluMetHisLeuAr 214  
Db 772 AGGTGACCTACCCCTTGGGTACCATCAGAAGACCTTGTATATGAAATGCAATTCGG 831  
QY 214 gGlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVa 234  
Db 832 TGGATTCAACAAAGCACAACTCAAGCAAGAACAAACACCCAGGAACCTTACATTGGTGT 891  
QY 234 lSerLysLeuAspTrrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHi 254  
Db 892 GTCAAGCTTGACCATCAAGGAACCTTGAGTGAACCTGTATAGAGTAAATGCCCTGCCA 951  
QY 254 sGluPheAsnGluLeuGluTrrSerThrSerSerSerLysMetAsnPheTrrGlyTrrSe 274  
Db 952 TCAGTTCAATAGCTAGTACTTACGCTCCCTTCGAGATGAACCTTCGCGGATATTC 1011  
QY 274 rThrIleAsnPhePheSerProMetThrArgTrrThrSerGlyGlyLysAsnCysGl 294  
Db 1012 CACAAATAAATTTTCTCCCAATGGCAAGATATTCCTCAGTGGCATAGAGACTCTGG 1071  
QY 294 yArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGl 314  
Db 1072 ATGTGTCGCATAAATGAATTTAAAGCTTTTGTAAAGGAGGCGCCCAACCGGGAAATGA 1131  
QY 314 uValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLe 334  
Db 1132 GGTGATCATGAGTGTGTCTTCAATCATACGCTGAGGTAAATGAGAAGGCCCAATATT 1191  
QY 334 uSerPheLysGlyValAspAsnThrThrTrrTrrMetLeuAlaProLysGlyGluPheTrr 354  
Db 1192 ATCCTTTAGGGGATAGATAATAGTACTACTACATGCTTGACCTTAAGGGAGAGTTTA 1251

QY 354 rAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIl 374  
Db 1252 TAAATATTCTGGTGTGGAAATACCTTCAATTTGAATCATCTAGTCCGCGGAATTTAT 1311  
QY 374 eValAspCysLeuArgTrrTrrValThrGluMetHisValAspGlyPheArgPheAspLe 394  
Db 1312 AGTGGATTGCTTGAGATACTGGTAAACAGAAATGCATGTTGATGTTTCGTTTGACCT 1371  
QY 394 uAlaSerIleMetThrArgLysSerSerLeuTrrAspProValAsnValTrrGlyAlaPr 414  
Db 1372 TGCATCTATATCACCAGAGGATCCAGTCTATGGGATCCAGTTAATGTGTATGGAATCC 1431  
QY 414 lIleGluGlyAspMetIleThrThrProLeuValThrProProLeuIleAspMe 434  
Db 1432 AATGGAGGTGACATGATTACGACAGGACACCTCTGTGTGCCCCACCTTATTGACAT 1491  
QY 434 tIleSerAsnAspProIleLeuGlyGlyValLysLeuIleAlaGluAlaTrrAspAlaGl 454  
Db 1492 GATTAGCAATGACCAATTTCTGGAAATGTCAAGCTCATTTGCTGAAGCATGGATGCAG 1551  
QY 454 yGlyLeuTrrGlnValGlyGlnPheProHisTrrAsnValTrrSerGluTrrAsnGlyLy 474  
Db 1552 AGGTCTCTATCAAGTTGGTCAGTTTCTCCTCAGTGAACGTTTGTTCAGTGGAAATGAAA 1611  
QY 474 sTyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyLysPheAl 494  
Db 1612 GTATCCGATACCGTGGTCAGTTTCATCAAGGCACAGATGGATTGCTGGTCTTTTCG 1671  
QY 494 aGluCysLeuCysGlySerProHisLeuTrrGlnAlaGlyGlyArgLysProTrrHisSe 514  
Db 1672 TGAATGCTATGTGGAGTCCACAGTTATATCCAGGCGAGGGGAGGAGCCCTTGGCACAG 1731  
QY 514 rIleAsnPheValCysAlaHisaspGlyPheThrLeuAlaAspLeuValThrTrrAsnLy 534  
Db 1732 TATCAACTTTGTTATGTGCACAGATGGATTACCTGGCTGATTGTTGTCATACATACATAG 1791  
QY 534 sLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTr 554  
Db 1792 CAAGTCAACTTCTCAATGGTGGAGCAACAGAGATGGGAAAAATCATAATCTTAGCTG 1851  
QY 554 pAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGl 574  
Db 1852 GAATTTGCGGAGGAGGAGAAATTTCAAGTCTGTCTCAGTCCGAGAAATTAAGGAAGGCA 1911  
QY 574 nMetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTrrMetGl 594  
Db 1912 AATGCGCAATTTCTTTGTTGTTCTTCTCAGGAGTTCCTCAATGTTCTACATGGG 1971  
QY 594 yAspGluTrrGlyHisThrLysGlyLysAsnAsnAsnThrTrrCysHisAspSerTrrVa 614  
Db 1972 CGATGAATATGGTCACACAAAGGAGGAGAACAAATCTGCTACTGCTCATGACCATTTAT 2031  
QY 614 lAsnTyrPheArgTrrAspLysLys---GluGlnTrrSerGluLeuHisArgPheCysCy 633  
Db 2032 CAATTTATTTCCGTTGGATAGGAAGGAACAACTCTCTGATTGTCAGATTCTGCGG 2091  
QY 633 sLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAl 653  
Db 2092 TCTCATGACCAAAATTCGCAAAAGAAATGTGAATCTCTTGGCTTGGAGACTTCCCGACTTC 2151  
QY 653 aLysArgLeuGlnTrrHisGlyHisGlnProGlyLysProAspTrrSerGluAsnSerAr 673  
Db 2152 AGAAGGTTTGAATGGACGCTCATCAGCCCGGAAGGCTGACTGTGTCAGAGCAAGCCG 2211  
QY 673 gPheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTrrValAlaPheAsnTh 693  
Db 2212 ATTCGTTGCTCTCACCATGAAGGACGAAACCAAGGCGGAGATCTACGTGGCTTCAACAC 2271  
QY 693 rSerHisLeuProAlaValGluLeuProGluAlaGlyArgArgTrrGluProVa 713  
Db 2272 CAGTCACCTTCCGTTGTTGTTGGGCTTTCAGAGGCTCTGGGTTCCGATGGAGCGCGT 2331

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QY 713 lValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAl 733
Db 2332 GGTGGACACGGCAAGAGGACCATATGACTTCTCCACCGATGGCTGCCAGATCGTGC 2391
QY 733 aLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTy 753
Db 2392 TGTACCGGTCTACCGAGTCTCTCTATTTCTCACTCACTCACTCTATCTATCTATGCTCAGCTA 2451
QY 753 rSerSerValIleLeuValLeuValLeuArgProAspVal 764
Db 2452 CTCCTCCATCATCTTGTATTGGCCCTGATGTC 2485

RESULT 6
US-09-938-842A-218
; Sequence 218, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 218
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-218

Alignment Scores:
Pred. No.: 0 Length: 2352
Score: 2895.50 Matches: 518
Percent Similarity: 81.08% Conservative: 82
Best Local Similarity: 70.00% Mismatches: 127
Query Match: 68.74% Indels: 14
DB: 9 Gaps: 4

US-09-674-817B-3 (1-764) x US-09-938-842A-218 (1-2352)
QY 29 GluAlaAlaThrLysValGluAspGluGlyGluGluAspGluProValAlaAlaLeu 48
Db 140 GAAGAGCAACCAAGCT-GAAATATCGCCGTAGTAGAGAAACCTCTTAAATCAGATAGA 198
QY 49 TyrAlaLeuGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 68
Db 199 TTTTATCTCCGAT-----GGACTTCTCTCCATTCGACCCACC 240
QY 69 AlaLeuAlaGlyValAsnPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeu 88
Db 241 GTCAGACGACGGCGTCAATTTCTGTTTACTCTACAACTCCGTTTCGCTACCATC 300
QY 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAsp 108
Db 301 TCTTGTATTTCTCTCCGATCTCCGTGAGACAAAGTGACGAGGAGGATTCAGCTTGAT 360
QY 109 ProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyGluLeuHisAsn 128
Db 361 CCATCAAGGATAGAACTGGCCATGTTGGCATGTGTTCTTGAGAGGAGATTCAAAGAT 420
QY 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148
Db 421 ATGTTGTATGTTATAGATTTGATGGCAAGTTTCTCTCTGAAAGGATTCATTTATGAT 480

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QY 149 ValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGluTyrGly 168
Db 481 TCCITCCAACTATTATTGGATCTTACGCAAGCAATTAAGCAGAGATGAGTTGGA 540
QY 169 ValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyr 188
Db 541 GTTTGGACCTGATGATAAATTGTTGGCTCAAAATGGCTGTATGGTACCCACCTCGTAG 600
QY 189 SerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIle 208
Db 601 GAAGAGTTTGATTGGGAAGGGATATGCAATCTGAAGCTTCCACAGAAAGATCTTTGTTATA 660
QY 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228
Db 661 TATGAATGCAATGTGCGAGGTTTACAAGGCATGAGTCTAGTAAATTAATTCCTCGGC 720
QY 229 ThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIle 248
Db 721 ACATACAGGGTGTTCAGAGAGCTTGACCAITTGAGGAGCTTGGGATAAATTGTATA 780
QY 249 GluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSer----- 266
Db 781 GAATTAATGCCATGTACGAGTTTAAATGAGCTGGAGTATTACAGCTACAATACGATTTG 840
QY 267 -----LysMetAsnPheTrpGlyTyrSerThrIleAsnPheSerProMetThr 283
Db 841 GGAGACCACAGGGTAAATTTTGGGGTTACTCTACCATTGGGTCTTCTCGCCCATGATC 900
QY 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
Db 901 AGATACGCATCAGCAACCTCTAACAATTTGCTGGACGACCCATAAATGAATTCAAAATT 960
QY 304 PheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHis 323
Db 961 CTTGTTAAGGAGGCACATAAAGAGGAATTAGGTAATCATGATGTCGCTTGAACAC 1020
QY 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThr 343
Db 1021 ACAGCCGAGGGAATGAAAAGGGCCCATTTTCTCATTTAGAGAGTTGTAACAGTGT 1080
QY 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363
Db 1081 TATTACATGCTTGTCCAAAGGCGAGTTCTATAAATATTATTCAGCTGTGTAATACATTC 1140
QY 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTrpValThr 383
Db 1141 AACTGCAATCATCTCTGGTGGCTCAATTCATATGATTCGATTCGCTGAGATATCGGTACA 1200
QY 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403
Db 1201 GAAATGCATCTTGACGGCTTCCGCTTTGATCTTGGTTCAATCATGTCNAGGACGACGAGC 1260
QY 404 LeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGly 423
Db 1261 CTTTGGATGACAGCCAATGTTTACGGGGCTGATGTAGAAGGTGACTTGTCTCACAACGTGT 1320
QY 424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGly 443
Db 1321 ACTCTTATTAGCTGCCCTCCAGTAAATGACATGATGAATGAATGATCCAATCTCCCGGT 1380
QY 444 ValIleLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGlyGlnPhePro 463
Db 1381 GTTAAAGCTAATAGCTGAAGCATGGGATCGGGTGGGCTGTACCAAGTTGGCATGTTTCCA 1440
QY 464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483
Db 1441 CACTGGGTATTGTGCTCTGAGTGAATGAAAGTTTCGGGATGTTCTGAGACAGTTTCATA 1500
QY 484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503
Db 1501 AAAGGCACCGATGCTTTTCTGCTGCTTTTGTGATGATGCTCTGTGGAAGCCCAATCTG 1560
QY 504 TyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGly 523

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Db 1561 TACCAG--GGAGGTAGGAAACCTTGGCACAGCATCAATTTATATGTGCGCATGATGGT 1617
Qy 524 PheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsn 543
Db 1618 TTTAGCTTGGCAGATTTAGTAACTTACCAACATAGAAATACTTGGCAATGGAGAGAG 1677
Qy 544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyPheAla 563
Db 1678 AATAATGATGGAGAGAAATCACAAATACAGCTGGAACCTGGAGAGAGAGAGCTTGGC 1737
Qy 564 ArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMet 583
Db 1738 AGTATCTCGTCAAGAGACTAAGGAAACGACAGATGCGGAATTTCTTTGTTTCCCTCATG 1797
Qy 584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603
Db 1798 GTTTCCTCCAGGTGTCCTCAATGATTTACATGGGAGATGAATATGGCCATACCTAAAGGGGA 1857
Qy 604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGlu 623
Db 1858 AACACAAACACGATTTGCCATGACAACTATATGAATTTTTCGGTGGGATAAAGGAA 1917
Qy 624 Gln--TyrSerGlnLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642
Db 1918 GAAGCACAATTCGACTTCTCAGATCTCGCGTATCTTATCAAGTTTCGTGATGAATGT 1977
Qy 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662
Db 1978 GAATCACTTGGCTTGAATGATTTCCCAACAGCAAGCGTCTCGAGTGGCATGGTCTTCT 2037
Qy 663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682
Db 2038 CTTGAGATCCCAATTTGGTCTGAAACAGTCTGATTTGTTGCAATTTTCTGCTGATCT 2097
Qy 683 ArgGlnGlyGluLeuTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702
Db 2098 GTGAGAAAGAAATCTATGTGGCTTCAACACAGCTCAATTTAGCCACACTTGTTCGCTA 2157
Qy 703 ProGluArgAlaGlyArgArgTrpGluProValValAspThrGlyLysProAlaProTyr 722
Db 2158 CCGAATAGGCGAGATACCGATGGGAGCCATTTGTAGACACAGCAACCGGACCTTAC 2217
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742
Db 2218 GATCGATACACCGGATCTCCAGAGAGAGAAACGGCGATGAAGCAGTATAGGCACCTC 2277
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762
Db 2278 TTAGATGCAAAATGTGTACCAATGCTCAGTTACTCATCTCATCTTCTTCCACCA 2337

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RESULT 7  
US-09-938-842A-218  
; Sequence 218, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 218

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; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-218

Alignment Scores:
Pred. No.: 0 Length: 2352
Score: 2895.50 Matches: 518
Percent Similarity: 81.08% Conservative: 82
Best Local Similarity: 70.00% Mismatches: 127
Query Match: 68.74% Indels: 14
DB: 11 Gaps: 4

US-09-674-817B-3 (1-764) x US-09-938-842A-218 (1-2352)

Qy 29 GluAlaAlaThrLysValGluAspGluGlyGluAspGluProValAlaGluAspArg 48
Db 140 GAAGAAAGCAACGAAGCT-GAAAAATATCGCGTAGTAGAGAAACCTCTTAAATCAGATAGA 198
Qy 49 TyrAlaLeuGlyGlyAlaCysArgValLeuAlaGlyMetProAlaProLeuGlyAlaThr 68
Db 199 TTTTATATCTCCAT-----GGACTTCTTCTCATTTCGACCCACC 240
Qy 69 AlaLeuAlaGlyGlyValAsnPheAlaValTyrSerGlyGlyAlaThrAlaAlaLeu 88
Db 241 GTCAGAGACGACGCGCTCAATTTCTCTGTTTATCTTACAACTCCGCTTCCGCTACCATC 300
Qy 89 CysLeuPheThrProGluAspLeuLysAlaAspArgValThrGluGluValProLeuAsp 108
Db 301 TGTCTGATTTCTCTCTCCGATCTCCGTGAGCAAAAGTACGAGGAGATTCAGCTTGAT 360
Qy 109 ProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyGluLeuHisAsn 128
Db 361 CCATCAAGGAATAGAACTGGCCATGTTGGCATGTTCTTTCGAGAGGAGATTTCAAAGAT 420
Qy 129 MetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAsp 148
Db 421 ATGTGTATGTTGTTATAGATTTGATGCAAGTTTCTCTTCGAGAGAGTCAATATTATGAT 480
Qy 149 ValSerAsnValValValAspProTyrAlaLysAlaValIleSerArgGlyGlyGly 168
Db 481 TCCTCCCAACATTTTATGATCTTACGCAAGGCAATATTAAGCAGAGATGAGTTGGA 540
Qy 169 ValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyr 188
Db 541 GTTTTGGGACCTGATGATAATTGTTGGCTCAATGGCGTGTATGTATGCTACCCATCCTGAG 600
Qy 189 SerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeuValIle 208
Db 601 GAAGAGTTTGTATGGGAGGGGATATGCATCTGAGCTTCCAGAGCTTCCACAGAAAGATCTTGTATA 660
Qy 209 TyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHisProGly 228
Db 661 TATGAAATGCATGTCGAGGCTTTTACAAGGCATGAGTCTAGTAAATTTGAATTTCCCTGGC 720
Qy 229 ThrPheIleGlyAlaValSerLysLysLysLysGluLeuGlyValAsnCysIle 248
Db 721 ACATACCAGGCTGTTGCAGAGAGCTTGACATTTGNAGAGGCTTGGGATAAATTTGATA 780
Qy 249 GluLeuMetProCysHisGluPheAsnGluLeuGlyTyrSerThrSerSerSer----- 266
Db 781 GAATTAATGCATGTCACGAGTTTAAATGAGTGGAGTATTAAGCTACATACAGTATTTG 840
Qy 267 -----LysMetAsnPheTrpGlyTyrSerThrIleAsnPhePheSerProMetThr 283
Db 841 GGAGACCACAGGCTAAATTTTGGGGTACTTACCAATGGGTTCTTCTCGCCCATGATC 900
Qy 284 ArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThr 303
Db 901 AGATACCAATCAGCAAGCTCTCAAAATTTTGTGTCGAGAGCCATTAATGAATTTCAAAT 960
Qy 304 PheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValValPheAsnHis 323

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Db 961 CTTGTTAAGGAGGCACATAAAACGAGGAATTGAGTAATCATGGATGCTGCTTTGAACAC 1020  
Qy 324 ThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheIleValAspAsnThrThr 343  
Db 1021 ACAGCCGAAGGGAATGAAAGAGGCCCAATTTCTCAITTAGAGGAGTTGATAACAGTGC 1080  
Qy 344 TyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPhe 363  
Db 1081 TATTACATGCTGCTCCAAAGGCGAGTCTATAATTAATTCAGGCTGTGTAATACATTC 1140  
Qy 364 AsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyrTrpValThr 383  
Db 1141 AACTGCAATCATCCTGTGGTGGTCAATTCATATTCGATTGCTGAGATATTGGGTACA 1200  
Qy 384 GluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSer 403  
Db 1201 GAAATCGATGTTGACGGCTTCGGCTTTGATCTTGGTTCATATGTCAGAGGAGCGAGC 1260  
Qy 404 LeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGly 423  
Db 1261 CTTTGGGATCGACCAATGTTACGGGGCTGATGAGAGGTGACTTGTCTCAACTGCT 1320  
Qy 424 ThrProLeuValThrProProLeuIleAspMetIleSerAsnAspProIleLeuGly 443  
Db 1321 ACTCTATTAGTGGCTCCAGTAATTCATGATGATGATGATGATGATGATGATGATGAT 1380  
Qy 444 ValLysLeuIleAlaGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPhePro 463  
Db 1381 GTTAAGCTAATAGCTGAAGATGGGATCGGGTGGCTGTACCAAGTTGGCATGTTTCCA 1440  
Qy 464 HisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIle 483  
Db 1441 CACTGGGGTATTGGTCTCAGTGAATGGAATGGAAATTTCCGGATGTTGTGAGAGAGTTCATA 1500  
Qy 484 LysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeu 503  
Db 1501 AAAGGCACCGATGGCTTTCTGGTGGCTTTTGTGATGCTCTGTGGAGGCCAATCTG 1560  
Qy 504 TyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGly 523  
Db 1561 TACCAG--GGAGGTAGGAAACCTTGGCACAGCATCAATTTTATATGTGCGCATGATGT 1617  
Qy 524 PheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsn 543  
Db 1618 TTTACGTTGGCAGATTAGTAATTTACAAATAGATGATGATGATGATGATGATGATGAT 1677  
Qy 544 AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAla 563  
Db 1678 AATAATGATGGAGAGAAATCACAAATACAGCTGGAATGTTGGAGAGAGGAGACTTTGCG 1737  
Qy 564 ArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheValCysLeuMet 583  
Db 1738 AGTATCTCGTGAAGAGACTAAGGAAACGACAGATGCGGAAATTTCTTTTTCCTCATG 1797  
Qy 584 ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603  
Db 1798 GTTTCCCAAGGTGCCAATGATTACATGGGAGATGATATGAGGATGATGATGATGATGAT 1857  
Qy 604 AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGlu 623  
Db 1858 AACCAACACACGCTATTGGCCATGACAACTATATGAATATTTTCGGTGGGATAAAGGAA 1917  
Qy 624 Gln---TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642  
Db 1918 GAAGACATCTTGACTTCTTCAGATTCCTGCGCTATTCCTATTCAGATTTTCGTGATGAT 1977  
Qy 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662  
Db 1978 GAATCACTTGGCTGAATGATTCCCAACAGCAAGAGCGTCTGAGTGGCATGCTTGTCT 2037  
Qy 663 ProGlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682  
Db 2038 CCTGAGATCCCAATTTGGTCTGAAACAGATGCTGATTTGTGATTTTCACTGGTGCATCT 2097

Qy 583 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702  
Db 2098 GTGAAGAAAGAAATCTATGTGGCTTCAACACCACTCATTTAGCCACACTGTTTCGCTA 2157  
Qy 703 ProGluArgAlaGlyArgTyrGluProValValAspThrGlyLysProAlaProTyr 722  
Db 2158 CCGAATAGCCAGGATACCGATGGAGCCATTTGTAGACAGCAGCAACCGAGCCCTTAC 2217  
Qy 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPhe 742  
Db 2218 GACTGCATAACACCGGATCTCCAGAGAGAGAAACCGCGATGAGAGCAGTAGTAGGCATTC 2277  
Qy 743 LeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuValLeuArgPro 762  
Db 2278 TTAGATGCAATATGTTACCAATGCTCAGTACTCATTCATCCATCTCTCTCTTCACCA 2337

## RESULT 8

US-10-425-114-19788  
; Sequence 19788, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)5  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 19788  
; LENGTH: 1866  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-045-C7\_FLI  
US-10-425-114-19788

Alignment Scores:  
Pred. No.: 0 Length: 1866  
Score: 2820.50 Matches: 506  
Percent Similarity: 94.05% Conservative: 31  
Best Local Similarity: 88.62% Mismatches: 33  
Query Match: 66.96% Indels: 1  
DB: 13 Gaps: 1

US-09-674-817B-3 (1-764) x US-10-425-114-19788 (1-1866)

Qy 195 GlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArg 214  
Db 1 GGTGACCTACCCCTGGGTGCTACCATCAGAGGACCTTGTATATGAAATGCAATTCGCT 60  
Qy 215 GlyPheThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaVal 234  
Db 61 GGATTCAAAAGCAACAATCAAGCAAGAAACACCCAGGAACCTTACATTTGCTGTG 120  
Qy 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254  
Db 121 TCAAGCTTCACCATCTAAAGGAACCTGGAGTGAACCTGTATAGAGCTAATGCCCTGCCAT 180  
Qy 255 GluPheAsnGluLeuGluTyrSerThrSerSerSerLysMetAsnPheTrpGlyTyrSer 274  
Db 181 GAGTTCATGAGCTAGAGTACTTCAGCTCCTCTTCGAAGATGAACCTTCGGGATATTC 240  
Qy 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294  
Db 241 ACATAAATTTTTCTCCCAATGGCAAGATATCTTCAAGTGGCATAAGAGACTCTGGA 300  
Qy 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314

Db	301	TTGTGGTGCATAAATGAATTTAAAGCTTTTGTAAAGGAGGCCCAAAACGGGGGAATTGAG	360	1381	GAACGGTTGAATGGCAGCGTCATCAGCCCGGGAAGCCTGACTGGTCAGAGGCAAGCCGA	1440	
Qy	315	ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu	334	Qy	674	PheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThr	693
Db	361	GTGATCATGGATGTTGTCTTCAATCATACAGCTGAAGGTAAAGAAAAGGCCCAATATTA	420	Db	1441	TTCTGTTGCTTCCACCATGAAGGACGAACCAAAAGGCGAGATCTACGTGGCCCTTCAACACC	1500
Qy	335	SerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyr	354	Qy	694	SerHisLeuProAlaValValGluLeuProGluArgAlaGlyArgArgTrpGluProVal	713
Db	421	TCCTTTAGGGGATAGATAATAGTACACTACTACATGCTTGACCTTAAGGAGAGATTTAT	480	Db	1501	AGTCACCTTCCGGTGTGTTGGCTTCCAGAGCGCTCTGGGTCCGATGGAGCGCGTG	1560
Qy	355	AsnTyrSerGlyCysGlyAsnThrPheAsnHisPheAsnHisProValValArgGlnPheIle	374	Qy	714	ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla	733
Db	481	AATTATCTGGTGTGGAAATACCTTCAATTGTATCATCTCTGTAGTCCGTGAATTTATA	540	Db	1561	GTGGACACCGCGCAAGGAGGACCATATGACTTCTCCACGATGGCTGCCACATCGTGT	1620
Qy	375	ValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeu	394	Qy	734	LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr	753
Db	541	GTGGATTGCTTGAGATACCTGGTAAACAGAAATGCATGTTGATGTTTCGTTTTCACCT	600	Db	1621	GTCCCGTGTACAGTCTCTCATTTCTCAACTCCAACTCTATCTATCTATCTAGCTCAGCTAC	1680
Qy	395	AlaSerIleMetThrArgGlySerSerLeuTyrAspProValAsnValTyrGlyValPro	414	Qy	754	SerSerValIleLeuValLeuArgProAspVal	764
Db	601	GCATCTATCTACTGACCCAGAGATGCGAGTCTATGGGATCCAGTTAATGTGTATGGAAGTCA	660	Db	1681	TCCTCCATCATCCTTGTATTGGCCCTGATGTC	1713
Qy	415	IleGluGlyAspMetIleThrThrGlyThrProLeuValThrProProLeuIleAspMet	434	RESULT 9			
Db	661	ATCGAAGGTGACATGATTACGACAGGACACCTCTGTGTCGCCACCACTTATTGACATG	720	US-09-850-936-1			
Qy	435	IleSerAspAspProIleLeuGlyValLysLeuIleAlaGluAlaTrpAspAlaGly	454	Sequence 1, Application US/09850936			
Db	721	ATTAGCAATGACCCCAATCTTGGAAATGTCAGCTCATGTCGAAGCATGGGATGCGAGA	780	Publication No. US20030167527A1			
Qy	455	GlyLeuTyrGlnValGlyGlnPheProHisTyrAsnValTrpSerGluTrpAsnGlyLys	474	GENERAL INFORMATION:			
Db	781	GGTCTCTATCAAGTGTGTCAGTTTCTCACTCGAAGCTTGTGTGTCAGATGGAATGGAAG	840	APPLICANT: Emmermann, Michael			
Qy	475	TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyClyPheAla	494	APPLICANT: Kossmann, Jens			
Db	841	TATCGGATACCGTGGCTGATTCATCAAGACACAGATGGATTTGCTGGTCTTTTCTCT	900	TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES			
Qy	495	GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyArgLysProTyrHisSer	514	FILE REFERENCE: GFB8			
Db	901	GAATGCTATGTGAAGATCCACAGTTATACAGGACGAGGGGAGGAGCCTTGGACAGT	960	CURRENT APPLICATION NUMBER: US/09/850,936			
Qy	515	IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys	534	CURRENT FILING DATE: 2001-05-08			
Db	961	ATCAACTTGTATGTGCACACGATGATTTACACTGGCTGATTTGGTCACATACATAAGC	1020	PRIOR APPLICATION NUMBER: US/09/187,124			
Qy	535	LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrp	554	PRIOR FILING DATE: 1998-11-05			
Db	1021	AGTACAACCTGTGCAATGTGAGGACACAGATGGGAAATCATATCTTAGCTGG	1080	PRIOR FILING DATE: 1997-05-06			
Qy	555	AsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln	574	PRIOR APPLICATION NUMBER: PCT/EP97/02292			
Db	1081	AATTGTGGGAGGAGAGAAATTGCAAGTCTGTGTCGCGAGATTAAGGAAGAGGCAA	1140	PRIOR FILING DATE: 1996-05-06			
Qy	575	MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly	594	NUMBER OF SEQ ID NOS: 2			
Db	1141	ATGCGCAATTTCTTTGTTGTTCTTATGTTTCTCAGGAGATTCCTGATTTGACAGATTC	1200	SOFTWARE: PatentIn Ver. 2.1			
Qy	595	AspGluTyrGlyHisThrLysGlyAsnAsnAsnThrTyrCysHisAspSerTyrVal	614	SEQ ID NO 1			
Db	1201	GATGATATGTTGACAAAGGAGGAGGAAACAATACGATCTGTCATGACCATATATGTC	1260	LENGTH: 2133			
Qy	615	AsnTyrPheArgTrpAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys	633	TYPE: DNA			
Db	1261	AATTATTTCCGTTGGGATGAAGGAGGAACAATCTCTGATTTGACAGATTCCTGCCGT	1320	ORGANISM: Solanum tuberosum			
Qy	634	LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAla	653	FEATURE:			
Db	1321	CTCATGACCAATTCGCAAGAGATGTGAAATCTCTTGGCTTGAGACTTCCGACTTCA	1380	NAME/KEY: CDS			
Qy	654	LysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTrpSerGluAsnSerArg	673	LOCATION: (2)...(1819)			
				OTHER INFORMATION: Clone: Iso5			
				US-09-850-936-1			
				Alignment Scores:			
				Pred. No.: 5,31e-309	Length: 2133		
				Score: 2612.00	Matches: 460		
				Percent Similarity: 86.86%	Conservative: 62		
				Best Local Similarity: 76.54%	Mismatches: 73		
				Query Match: 62.01%	Indels: 7		
				DB: 10	Gaps: 2		
				US-09-674-817B-3 (1-764) x US-09-850-936-1 (1-2133)			
Qy	166	GluTyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIlePro	185				
Db	1	GAATTCGGACGAGGCGCCAGGAT--GATTGTGGCCCCCATGCGCAGCATGTACCT	58				
Qy	186	LeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAsp	205				
Db	59	TCGTCTCTCATCAGTTGATTGGGAAGGAGATCTATTACTGAAGTTTCCACAGAGAT	118				
Qy	206	LeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGlu	225				
Db	119	CTTGTAATCATGAATGATGTTCTGTGGATTTTACAAATCATGAGTCGAGTGAACAAA	178				

Qy	226	HisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyVal	243
Db	179	TATCCTGGTACTTACCTTGGTGTGTGGAGAACTTGATCACTTGAAGAACTTGGTGT	238
Qy	246	AsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSer	265
Db	239	AACTGTATAGAGCTAATGCCCTGTCCAGAGTTCATAGAGCTGGAGTACTATAGTTTATAAC	298
Qy	266	Ser-----LysMetAsnPheNtrpGlyTyrSerThrIleAsnPhePheSer	280
Db	259	TCTGTATTGGGGAGCTACAGGTTTAACTTTTGGGGCTATCTTACGTTCATTTCTTTCT	358
Qy	281	ProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAspAlaIleAsnGlu	300
Db	359	CCAAATGGGAAGATACCTGCTGCTGGTCTAAGTAATTCCGGCTCGGTGCAATAAACGAA	418
Qy	301	PheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIleLeuAspValVal	320
Db	419	TTTAAAGTATCTTGTCAAGGAAGCACATAAAGCTGAATCGAGGTATCATGGATGTGGT	478
Qy	321	PheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPheLysGlyValAsp	340
Db	479	TTCAATCACACTGCTGAAGGAAATGAAATGGTCCCACTACTATCATTTAGAGGCATTGAC	538
Qy	341	AsnThrThrTyrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyrSerGlyCysGly	360
Db	539	AACAGTGTGTTTATACGCTAGCTCCTAAGGGTGAATTTTCAACTACTCAGGATGTGGA	598
Qy	361	AsnThrPheAsnCysAsnHisProValValArgGlnPheIleValAspCysLeuArgTyr	380
Db	599	AATACCTTCAACTGTAAATAATCCCACTGCTACGTCAATTTATAGTGGATTGCTTCAGATAT	658
Qy	381	TrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSerIleMetThrArg	400
Db	659	TGGGTACCGAAATGCACGTAGATGGCTTCGGCTTTGATCTTGTCTTATCCTTACAAGA	718
Qy	401	GlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGluGlyAspMetIle	420
Db	719	AGTAGCAGCTCGTGGAAATGCTGTAATGTCTATGGAAATTCAAATTGACGGTGACATGATC	778
Qy	421	ThrThrGlyThrProLeuValThrProProIleLeuAspMetIleSerAsnAspProIle	440
Db	779	ACCACAGCACTCCTCTCACAGGCCACCAATGTATTGATATGATAGCAATGATCCCAATA	838
Qy	441	LeuGlyGlyValLysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGly	460
Db	839	CTTAGTGGAGTAAAGCTTATAGCTGAGCATGGGATTGTGGAGGCCTTTACCAAGTTGGC	898
Qy	461	GlnPheProHisTrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArg	480
Db	899	ATGTTTCCGCACTCGGGGTATCTGTCGGAGTGGGAACGAAAGTACCCTGACATGGTACGT	958
Qy	481	GlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuGlyGlySer	500
Db	959	CAGTTTCATCAAGCACATGATGGGTTTCTGGGGCTTTTGTGTAATGCCTTTGTGGGAAGC	1018
Qy	501	ProHisLeuTyrGlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAla	520
Db	1019	CCAAATCTATACCAGAAAGGAGGAAGAAACCAATGGAACAGTATAAATTTCTGTGTGCC	1078
Qy	521	HisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsn	540
Db	1079	CACGATGGTTTTACTTTGGCTTGATTTAGTGACATACAAACATAAACAAATTTGGCAAT	1138
Qy	541	GlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGly	560
Db	1139	GGAGAGGACAAACAAAGATGGGCAATCACATAATAGTTGGAATTTCTGGCAGGAAGGA	1198
Qy	561	GluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheVal	580
Db	1199	CAATTTGCCAAGTATCTTTGTGAAGAAATGAGGAAAGACAAATGCGGAATCTTCTTCCTC	1258

QY	581	CysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThr	600
Db	1259	TGCGCTTATGGTTTCCCAAGGTTTCCCATATATATATATGGGTGAATATGGTCACACT	1318
QY	601	LysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAsp	620
Db	1319	AAGGAGGAAACAACAACAGTATTGCCATGACAATATATAATTACTTCCGTGGGAT	1378
QY	621	LysIys---GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArg	639
Db	1379	AAGAAGGATGAATCTTCATCTGATTTTTTTCAGATTTTTTTCGGCGCTCATGCACCAATTC	1438
QY	640	LysGluCysGluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTyrHis	659
Db	1439	CATGAATGTGAATCACTGGGATTAGATGGTTTCCCTACACAGAAAGGCTGCAATGGCAT	1498
QY	660	GlyHisGlnProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPheSerMet	679
Db	1499	GGTCACACTCTCTAGAACTCCAGATTTGCTCTGAAACAAGTCGATTCGTTGCATTTACACTG	1558
QY	680	LysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaVal	699
Db	1559	GTCCACAAAGTGAAGGAGAACTATATATTGCTTTAACCCGAGCCATTTCCTGTAAACG	1618
QY	700	ValGluLeuProGluArgAlaGlyArgArgTyrPgluProValValAspThrGlyLysPro	719
Db	1619	ATTACACTTCCAGAAAAGCCCTGGTTATAGATGCGAGCCGTTTGTGGACACAGGCAACCA	1678
QY	720	AlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPhe	739
Db	1679	GCACATTGACTCTTCAGACAGCATGTTCTCTGAGAGAGACAGCAGCCAAACAATAT	1738
QY	740	SerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeuVal	759
Db	1739	TCTCATTTTCTGGACGGCAACCAAGTATCCGATTCAGTTATTCATCCATTATCTTTTA	1798
QY	760	Leu 760	
Db	1799	CTA 1801	
RESULT 10			
US-10-425-114-6193			
; Sequence 6193, Application US/10425114			
; Publication No. US20040034888A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Screen, Steven E			
; APPLICANT: Tabaska, Jack E			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; FILE REFERENCES: 38-21(53313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 6193			
; LENGTH: 1830			
; TYPE: DNA			
; ORGANISM: Glycine max.			
; FEATURE:			
; OTHER INFORMATION: Clone ID: 700556474_FLI			
US-10-425-114-6193			
Alignment Scores:			
Pred. No.:		7.03e-253	Length: 1830
Score:		2153.50	Matches: 381
Percent Similarity:		88.03%	Conservative: 38
Best Local Similarity:		80.04%	Mismatches: 56
Query Match:		51.13%	Indels: 1
DB:		13	Gaps: 1

US-09-674-817B-3 (1-764) x US-10-425-114-6193 (1-1830)

QY 289 GlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAla 308  
Db 4 GGCATACGAACTGTGGCCAGGATTAATGAATTAATCTCTGATCAAGAGCG 63

QY 309 HisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsn 328  
Db 64 CACAAACGAGGAATAGAGTCATCATGATGTTGTTTCAATCATACAGCTGAGGGGAAT 123

QY 329 GluAsnGlyProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAla 348  
Db 124 GAGATGGTCCCATTTATTTCTTCAGAGGTGCGACACAGTATGTTATCATGTAGCA 183

QY 349 ProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisPro 368  
Db 184 CCCAAGGGGAGTCTCTATAACTTATTCAGGATGCGAACACAGCTTCAATTCGAACCATCCA 243

QY 369 ValValArgGluPheIleValAspCysLeuArgTyrTyrValThrGluMetHisValAsp 388  
Db 244 GTGTGCGCAATTTATAGTTGCTTGAAGTATGCTTGAAGTATGCTTGAAGTATGCTTGAAG 303

QY 389 GlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrAspProVal 408  
Db 304 GGTTCCTGCTTGTGCTTCTATATGACGAGGATGAGTCTCTGCGATGGAGCT 363

QY 409 AsnValTyrGlyValProIleGluGlyAspMetIleThrThrGlyThrProLeuValThr 428  
Db 364 AATGATTTTGGTCTCCCAATGAAGTACTTGTGACACAGGAAACCCCTCTAAGCAGC 423

QY 429 ProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIleLeuAla 448  
Db 424 CCACCATTAATTTGACTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 483

QY 449 GluAlaTyrPheAlaGlyLeuTyrGlnValGlyGlnPheProHisThrPheAsnValThr 468  
Db 484 GAAGCTGGGATGCTGCTGCTCTATCAAGTGTGCTTCTCCCTCACTGGGGTATTTGG 543

QY 469 SerGluTyrAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGly 488  
Db 544 TCAGATGGAATGGGAGTATGACACAGGTCGCTGCTTATCAAGGATGACATGTC 603

QY 489 PheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGly 508  
Db 604 TTTCGTGGAGCTTTGCTGAATGCTTTGCTGAGTCTCTATTAATTTATCAAGGAGGGA 663

QY 509 ArgLysProThrPheIleSerLeuAsnPheValCysAlaHisAspGlyPheThrLeuAlaAsp 528  
Db 664 AGAAACCCGTGGATGATTAATTTGATGCGCTCATGATGGGTTCTCTAGCTGAT 723

QY 529 LeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGlu 548  
Db 724 TTGGTGACCTATAACAAAGAAATTAATTTGTCATATGGAGAGACAAATATGATGAGAA 783

QY 549 AsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLys 568  
Db 784 AATCATATAATATAGCTGGAACTGCGACAGGAGGGGAGTTTGTCAAGTACCTTCGGGTGAG 843

QY 569 ArgLeuArgLysArgGlnMetArgAsnPheValCysLeuMetValSerGlnGlyVal 588  
Db 844 AATTCAGGAACAGCAATAGCGAATTTTCTCTCTCATGTTTCTCCAGGAGGT 903

QY 589 ProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyr 608  
Db 904 CCAATGATATATATGGCGCATGAATGATGACACACAAAGAGGAGAAATAACAAATACCTAT 963

QY 609 CysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluGln---TyrSerGlu 627  
Db 964 TGTACGATTAATTTATCATATTTTCTCAATGGGACAAAAGAGAAATCTCTCATCAGAC 1023

QY 628 LeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeu 647  
Db 1024 TTCTTCAGATTTGTGCTCTATGACTAAGTTCCCGCAGGAATGTGAATCGCTAGGCTTA 1083

QY 648 GluAspPheProThrAlaLysArgLeuGlnTyrHisGlyHisGlnProGlyLysProAsp 667  
Db 1084 GCTGACTTCCCAACCTCTGAGAGGCTGAGTGGCATGGTCAATTCCTGGAAAGCCAGAC 1143

QY 668 TrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGlu 687  
Db 1144 TGGTCTGAAACACGCGCTTTTGTGGTCTGACCATGGTAGATTCAAGTGAAGGAGAAATA 1203

QY 688 TyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly 707  
Db 1204 TACATTCCTTCAATATGATGATCATTTACCTTTACAGTGTACCTTCCCGAGCGTCTGGA 1263

QY 708 ArgArgTyrGluProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAsp 727  
Db 1264 TACAAATGGAACTCTTGTAGACACACAGCCTACACCATATGATTTCTCACTCT 1323

QY 728 AspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeu 747  
Db 1324 GACCTTCCTGGAAGAGATATTCATACACAGTATGCTCAGTTCTGACGCCAATATG 1383

QY 748 TyrProMetLeuSerTyrSerSerValIleLeuValLeuArgProAsp 763  
Db 1384 TATCCCATGCTTATGTTATTTCTTCATTTCTTCCTTCCTGCGCATCCAGAT 1431

## RESULT 11

US-10-424-599-11817  
; Sequence 11817, Application US/10424599  
; Publication No. US20040031072A1

; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)/B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 11817  
; LENGTH: 2052  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_110679C.1

US-10-424-599-11817

Alignment Scores:  
Pred. No.: 8,496-253 Length: 2052  
Score: 2153.50 Matches: 381  
Percent Similarity: 88.03% Conservative: 56  
Best Local Similarity: 80.04% Mismatches: 56  
Query Match: 51.13% Indels: 1  
DB: 13 Gaps: 1

US-09-674-817B-3 (1-764) x US-10-424-599-11817 (1-2052)

QY 289 GlyIleLysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAla 308  
Db 4 GGCATACGAACTGTGGCCAGGATTAATGAATTAATCTCTGATCAAGAGCG 63

QY 309 HisLysArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsn 328  
Db 64 CACAAACGAGGAATAGAGTCAATCATGATGTTGTTTCAATCATACAGCTGAGGGGAAT 123

QY 329 GluAsnGlyProIleLeuSerPheLysGlyValAsnThrThrTyrTyrMetLeuAla 348  
Db 124 GAGATGGTCCCATTTATTTCTTCAGAGGTGTCGACACAGTATGTTATCATGTTAGCA 183

QY 349 ProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisPro 368  
Db 184 CCCAAGGGGAGTCTCTATAACTTATGAGGATGCGAACACAGTCTCAATTCGAACCATCCA 243

QY 369 ValValArgGlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAsp 398  
Db 244 GTTGTGGCAACAATTTATAGTTGCTGCTTAAGATAATTGGTAACACAAAATGCACGGAT 303  
QY 389 GlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspProVal 408  
Db 304 GGTGTTTCGCTTTCATCTTCTCTTATATGACACAGGATGACAGTCTCTGGGATGGAGCT 363  
QY 409 AsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThr 428  
Db 364 AATGTAATTTGGTGCTCCAAATAGAAAGGTGACTTGTTCACACACAGAAACCCCTCTAAAGCAGC 423  
QY 429 ProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIleLeuAla 448  
Db 424 CCACCAATTAATGACTGTGATCAGTAACGATCCTATATCTTGTGGAGTGAAGTTATAGT 483  
QY 449 GluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTrp 468  
Db 484 GAAGCTGGGATGCTGGTGCCCTTATCAAGTTGGCACTTCCCTCACTGGGCTATTGG 543  
QY 469 SerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGly 488  
Db 544 TCAGATGGAATGGGAAGTATAGACACAGGTGGCCCTGTTTATCAAGGTACAGATGC 603  
QY 489 PheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyGly 508  
Db 604 TTTGCTGGAGCTTTGCTGAATGCCCTTGTGGAGTCCTAAATTTATATCAGGAGGAGGA 663  
QY 509 ArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAsp 528  
Db 664 AGAAACCGTGGCATAGTATTAACTTTGTATGGCTCATGATGGGTTCACCTACTGCTGAT 723  
QY 529 LeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGlu 548  
Db 724 TTTGTCACCTATAACACAAAGATAATTTGTCAATGGAGAGACAAATAATGACGAA 783  
QY 549 AsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValIys 568  
Db 784 AATCATATAATAGCTGGAACTGGCGACAGGAGGGGGAGTTTGTGATACCTCGGTGAAG 843  
QY 569 ArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyVal 588  
Db 844 AAATTGAGGAACGACCAATCGGAAATTTTTCTCTCATGCTTCCACGGAGGTT 903  
QY 589 ProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyr 608  
Db 904 CCAATGATATATATGGCGATGAATATGACACACAAAAGGAGGAAATAACAATACCTAT 963  
QY 609 CysHisAspSerTyrValAsnTyrPheArgTyrAspLysLysGluGln---TyrSerGlu 627  
Db 964 GTTCAGATATATATCATTAATTTACTTCCAATGGGACAAAAGGAAAGATCCTCATCAGAC 1023  
QY 628 LeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeu 647  
Db 1024 TTCTTCAGATTTTGTGCTTATGACTAAGTTCCGCGAGGATGATGATCCTAGGCTTA 1083  
QY 648 GluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAsp 667  
Db 1084 GCTGACTTCCCAACCTCTGAGAGGCTGCAGTGGCATGTGCTCATTTTCTCGGAAAGCCAGAC 1143  
QY 668 TrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyLysIle 687  
Db 1144 TGGTCTGAACACGACCGTTTGTGCTGTACCATGTTAGATTACGTGAAGGGAGAAATA 1203  
QY 688 TyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuProGluArgAlaGly 707  
Db 1204 TACATTGCTTCAATGATGATGATTTACCTTTACAGATTACCTTTCGCGGAGCGTCTGGA 1263  
QY 708 ArgArgTrpGluProValValAspThrGlyLysProAlaProTyrAspPheLeuThrAsp 727  
Db 1264 TACAATGGGAACCTCTGTGTAGACACAGCAGGCTTACCATATGATTTCTCTCACTCCT 1323

QY 728 AspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeu 747  
Db 1324 GACCTTCCTGGAAGAGATATTGCCATACACAGATATGCTCAGTTTCTGACGCCAATATG 1383  
QY 748 TyrProMetLeuSerTyrSerValIleLeuValLeuArgProAsp 763  
Db 1384 TATCCATGCTTAGTTATTCTTCATTATCTCTTGCGCATTCAGAT 1431  
RESULT 12  
US-10-369-493-26385  
; Sequence 26385, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 26385  
; LENGTH: 2124  
; TYPE: DNA  
; ORGANISM: Synecchocystis sp.  
US-10-369-493-26385  
Alignment Scores:  
Pred. No.: 1,36-189 Length: 2124  
Score: 1636.50 Matches: 342  
Percent Similarity: 60.20% Conservative: 77  
Best Local Similarity: 49.14% Mismatches: 216  
Query Match: 38.90% Indels: 61  
DB: 16 Gaps: 16  
US-09-674-817B-3 (1-764) x US-10-369-493-26385 (1-2124)  
QY 56 ArgValLeuAlaGlyMetProAlaProLeuGlyAlaThrAlaLeuAlaGlyGlyValAsn 75  
Db 46 AAATCGCGCTGTGCCAGCCCTTCCCTTTGGGCCACCATTTGTCGGCGGGGAGTTAAT 105  
QY 76 PheAlaValTyrSerGlyGlyAlaThrAlaAlaLeuCysLeuPheThrProGluAsp 95  
Db 106 TTTTCCATTACTCTAGCCATAGCCGCTTGACCTAGTACTGTC-----GAG 156  
QY 96 LeuLysAlaAspArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGly 115  
Db 157 AAGCGGGCTCCCGACGCCCTTTGTGGAGATTCCTTT---CCAGAACTTTTCGCATGGT 213  
QY 116 AsnValTrp---HisValPheIleGluGlyGluLeuHisAsnMetLeuTyrGlyTyrArg 134  
Db 214 AATGCTATTGCAATGCTGTGTGTTTGACCTGGATTTTGAGAAATCTGGAATACCGCTATCGC 273  
QY 135 PheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValVal 154  
Db 274 ATGAGAGGCCCAATAACTTCCAGAGGCCCATTTGTTTGCACCCAGTAAGTTCCTTCT 333  
QY 155 AspProTyrAlaLysAlaValIleSerArgGlyGlyTyrGlyValProAlaArgGlyAsn 174  
Db 334 GATCCCTACGCCAAAGTGTGCTGCGCGGATGTTTGGGGCACCCACCAATTCGGAC 393  
QY 175 AsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGlu 194  
Db 394 GATATTAT---CAACACCGGGGCCGC-----CTCAGCTTTGACAAATTTGATTGGGAA 444  
QY 195 GlyAspLeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArg 214  
Db 445 AACGATTTCCCTCGGATGTTCCCTTCGAAGACATGCTCATTTATGAATGATGTCGCG 504

[illegible]

RESULT 13  
 US-10-437-963-39232/c  
 ; Sequence 39232, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TIME OF INVENTION: Plants and Uses Thereof for Plant Improvement

```

; FILE OF INVENTION: 38-21(53221)B
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 39232
; LENGTH: 2729
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT4530_42793C.1
US-10-437-963-39232

Alignment Scores:
Pred. No.: 5 24e-179 Length: 2729
Score: 1553.50 Matches: 343
Percent Similarity: 56.75% Conservative: 111
Best Local Similarity: 42.88% Mismatches: 258
Query Match: 36.88% Indels: 88
DB: 17 Gaps: 22
US-09-674-817B-3 (1-764) x US-10-437-963-39232 (1-2729)

```

QY 2 GlyProAlaProArgLeuArgArgTrpArgProAsnAlaThrAlaGlyLysGlyValGly 21  
DB 2694 GGGCGGCTCCG-----TGGAAAGGTGGGTGGCGAGCATCGGCTTCGGG 2647  
QY 22 GluValCysAlaAlaValValGluAlaAlaThrLys----- 33  
DB 2646 GAC-----CGGTCTGGGCTCAGAGCGGTGTTCTGGAAGCGCAGGTTAGCGGATTTGATTTC 2593  
QY 34 ---ValGluAspGluGluGluAspGluProValAlaGluAspArgTrpAlaLeuGly 52  
DB 2592 TGTACGAAGCACCGCGGAGAGCTCAGAACGGGACCGTGGGAGAGCATGCCAGGA 2533  
QY 53 -GlyAlaCys-----ArgValLeuAlaGlyMetProAl 63  
DB 2532 AAGAGGATGACAAATGTCTGATACTGAAATGCCATTTAAATATTCTCTGGTAAAGCCTT 2473  
QY 63 aProLeuGlyAlaThrAlaLeuAlaGlyValAsnPheAlaValTyrSerGlyAl 83  
DB 2472 CCCATTAGGAGTCTCAAGTTCAAGCGGCTGAACTTCGCACATTTCTCTCAGCATGC 2413  
QY 83 aThrAlaAlaLeuCysLeuPheThrPro-----GluAspLeuLysAlaAs 99  
DB 2412 TTCTTCTGTCTCATTTCTGTTAAAGCTTCTGGAGGGGAACTGAAGATGAGAAAGGTGC 2353  
QY 99 pArgValThrGluGluValProLeuAspProLeuMetAsnArgThrGlyAsnValTrpHi 119  
DB 2352 AGATGTTTCGAGTTGTT---TTAGACCAGCAGAAAGAACAACTGGGGATATATGGCA 2296  
QY 119 sValPheIleGluGly---GluLeuHisAsnMetLeuTyrGlyTrpArgPheAspGlyTh 138  
DB 2295 TGTGATAGTGGAGGGCTTGCTGCTTCTGTTCTTTATGGTATCGTGTGGTGGCCC 2236  
QY 138 rPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValValAspProTyrAl 158  
DB 2235 TCAAGGATGGGACCAAGGCCATAGATTGTATGACGACACTGTTCTTCTGGACCTTATGC 2176  
QY 158 aLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsnAsnCysTrpPr 178  
DB 2175 AAAATTAGTTCTGTCGAAAGTACTTTGGGTTGCTGAAGAGAAGTCAAGC----- 2124  
QY 178 oGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuPr 198  
DB 2123 -CAGCATTTTGGAAATATGATTTTGATAGCTCTCCTTTGATTGGGTGATGACTACAG 2065  
QY 198 oLeu---ArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPheTh 217  
DB 2064 GCTTCGAATTGCTCGGCGAGATCTAGTCATATGAAATGAACGCCGCGTTCAC 2005  
QY 217 rLysHisAspSerSerAsnValGluHisPro-----GlyThrPheIleGlyAlaValSe 235  
DB 2004 CGCGGATGAGTCAAGTGGCTTTGATTCGACTTCTCGTGAAGCTATCTTGGTCTCATGA 1945  
QY 235 rLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGl 255  
DB 1944 TAAATATCCCTCATTTGCTGGAACTTGGCGTTAATGCAGTGAACACTCTCTCTGTTTGA 1885  
QY 255 uPheAsnGluLeuGluTyr-----SerThrSerSerSerLysMetAsnPheTr 271  
DB 1884 GTATGATGAGCTGGAAATCAAGAGGTACCCCAAGGAGGACCATGTTCAATACATG 1825  
QY 271 pGlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLy 291  
DB 1824 GGGCTATTCTACGATAAACTTTTTCGCCATGAGCGGTTATGCTAGTGGCGGTGGTG 1765  
QY 291 sAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysAr 311  
DB 1764 ACCAGTGGCT-----GCTTCCAAAGAGCTCAAGCAGATGGTCAAGAAATGCTATAAGC 1711  
QY 311 gGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGl 331  
DB 1710 TGGCATAGAGGTTATTCTTGGATGTTGTTTACAAACCATCAAAATGAGCGGATGATGCTCA 1651  
QY 331 yProIleLeu---SerPheLysGlyValAspAsnThrThrTyrTyrMet-----LeuAl 348

DB 1650 CCCGTATATGACTCTTTCCTGGCATGTATGAAAGGTCTATTACATGTTAGACCTGAA 1591  
QY 348 aProLysGlyGluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisPr 368  
DB 1590 CAAAAATCTGAACCTACTGAACCTTCTCAGGCTGGGGAATACACTGAACCTCAACCACTCC 1531  
QY 368 oValValArgGlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAs 388  
DB 1530 TGTGTCAAGAGCTCATCTTGACAGCTTGAGACACTGGGTTGAGGAGTATCATACATAGA 1471  
QY 388 pGlyPheArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspProVa 408  
DB 1470 TGGATTTGCAATTGACCTTGCAAGTGTCTTGTTCGTGGACACAGAT----- 1425  
QY 408 lAsnValTyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValTh 428  
DB 1424 -----GGTTGTCTCTTGATGC 1408  
QY 428 rProProLeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValLysLeuIleAl 448  
DB 1407 ACCTCCACTCATCAAGGAAATTCCAAAGATGCTGTTATTATCTAGATGTAAGATCATTCG 1348  
QY 448 aGluAlaTrpAspAlaGlyLeuTyrGlnValGlyGlnPheProHisTrpAsnValTr 468  
DB 1347 TGAACCTTGGGATTGCGCGGCTTATCTCTGAGGCGGTTTCCCTAACTGGGACAGGTG 1288  
QY 468 pSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLysGlyThrAspGl 488  
DB 1287 GGCTGAATGGNACGGCAATACAGAGATGATCTTCGAAGATTATTAAAGGTGACCTGG 1228  
QY 488 yPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyL 508  
DB 1227 TATCAAGGGGTGTTTCGACTCTGTCTGGATCTGCTGATCTCTATCAGGTGAACGA 1168  
QY 508 yArgLysProTrpHisSerIleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAs 528  
DB 1167 GCGAAGCCCTTACCATGGTGTAATTTGTGATTGTCACATGATGGATTACTTATGTGA 1108  
QY 528 pLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyL 548  
DB 1107 CCTTGTCTTACAACTTAAAGCAATGATGCTTAATGGAGAGGTGGCTGTGATGATG 1048  
QY 548 uAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAlaArgLeuSerValLy 566  
DB 1047 CAATGACAATTTAGCTGGAACTGTGGTGTGAAGGAGAAACAAATGATCTGAATGTGTT 988  
QY 568 sArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetValSerGlnGlyVa 588  
DB 987 AAGTCTCGCTTCAAGACAAATGAAACTTCCATGTAGCTTTAATGATTTCTCAGGCGAC 928  
QY 588 lProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTy 608  
DB 927 CCCAATGATGTTGATGGCGCATGATATGTCATACACGTTATGGGAACAAACAATAGCTA 868  
QY 608 rCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGluGlnTyrSerGluLe 628  
DB 867 TGGNATGATACCTTTCATGATATAATTTCCATGGGACAGTTGGAAACAAAGAGAGATGG 808  
QY 628 uHis---ArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLe 647  
DB 807 CCATTTCCAGGTTTTCTCAGAGATGATAAAGTTTCGTCACAGCAACCAATATTAAAGACG 748  
QY 647 uGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGlnProGlyLysProAs 667  
DB 747 AGACAGGTTTTCTTAAATAAAACGATGTCACCTGGCAC-----GAGGATTG 703  
QY 667 pTrp---SerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGln---G 685  
DB 702 TTGGGAGAACCCGAAAGCAAAATTTTGGCAATTCACAGTACATGATCAACAATCTCGTGG 643  
QY 685 yGluIleTyrValAlaPheAsnThrSer-----HisLeuProAlaValValGluLeuPr 703



Db 642 AGATATCTATTGGCAATTCATGACATGACTATTTTGTGGACGCTGTAATTCCTCCACC 583  
 QY 703 ogluargAlaGlyArggTgTpGluProValValAspThrGlyLysProAlaProTyrAs 723  
 Db 582 ACCACAC---CATAAATGTTGAACCGTGTGTGTGATACCAACCTGGGAATCACCAATGA 526  
 QY 723 pPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLe 743  
 Db 525 TATTGTACAGAAAGGGTGCCA-----TT 502  
 QY 743 utyrSerAsnLeuTyrProMetLeuSerTyrSerValIleLeuValLeuArgPro 762  
 Db 501 TACAGGACCAAAATACAGAAATGCTCCATCTCTCCATTTCTGCTCAAGGCAAGCCT 444

RESULT 14  
 US-10-425-114-20367  
 ; Sequence 20367, Application US/10425114  
 ; Publication No. US2004003488A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yinhua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 20367  
 ; LENGTH: 1198  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3180-047-B3\_FLI  
 US-10-425-114-20367

Alignment Scores:  
 Pred. No.: 2,75e-176 Length: 1198  
 Score: 1526.50 Matches: 279  
 Percent Similarity: 88.82% Conservative: 15  
 Best Local Similarity: 84.29% Mismatches: 19  
 Query Match: 36.24% Indels: 19  
 DB: 13 Gaps: 2

US-09-674-817B-3 (1-764) X US-10-425-114-20367 (1-1198)  
 QY 452 AspAlaGlyLeuTyrGlnValGlyGlnPheProHisTyrAsnValTyrSerGluTyr 471  
 Db 3 GATCGAGGAGTCTATCAAGTTGTCAGTTTCTCTCACTGGACGTTTGGTCAAGATGG 62  
 QY 472 AsnGlyLys----- 474  
 Db 63 AATGGAAA-GGCCAACCTTAGAGTATGTTTCAACAATAGCCTCACTGACCAATAG 121  
 QY 475 TyrArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyPheAla 494  
 Db 122 TATCGGATACCGTGCCTCAGTTTCATCAAAAGGCACAGATGGATTTGCTGGTCTTTGCT 181  
 QY 495 GluCysLeuCysGlySerProHisLeuTyrGlnAlaGlyLysArgLysProThrHisSer 514  
 Db 182 GAATGCTATGTGGAAGTCCAGTTATACACAGCGGGGGGAGGAGCCTTTGGCAGAT 241  
 QY 515 IleAsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValThrTyrAsnLys 534  
 Db 242 ATCAACTTTGTATGTGCACACAGATGATTTACATCGCTGATTTGTCACATACATAGC 301  
 QY 535 LysTyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyr 554  
 Db 302 AAGTACAACCTTGTCAAATGTTGGAGCAACAGAGATGGGGAATCATATCTTAGCTGG 361

QY 555 AsnCysGlyGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGln 574  
 Db 362 AATTGTGGGAGGAGGAGAAATTTGCAAGTCTGTCACTCCGAAGATTAAAGGAAGAGGCAA 421  
 QY 575 MetArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGly 594  
 Db 422 ATCGGCAATTTCTTTGTTGTTTATGTTTCTTCAGGGAGTTCCAAATGTTCTACATGGC 481  
 QY 595 AspGluTyrGlyHisThrLysGlyGlyAsnAsnAsnThrTyrCysHisAspSerTyrVal 614  
 Db 482 GATGAATATGGTCACAAAGGAGGAGAAACAATACATGCTACTGCAATGACCATTTATGTC 541  
 QY 615 AsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCys 633  
 Db 542 AATTATTTCCGTTGGATTAAGAAGGAACAATCTCTGATTGTGACAGATTTCTGCCGT 601  
 QY 634 LeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeuGluAspPheProThrAla 653  
 Db 602 CTCATGACCGAATTCGCAAAAGAAATGTGAATCTCTTGGCCTTGAGGACTTCCGACTTCA 661  
 QY 654 LysArgLeuGlnThrHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArg 673  
 Db 662 GAACGGTTGAAATGGCACCGTCACTCAGCCCGGGAAGSCCTGCTGGTCAGAGCAAGCGA 721  
 QY 674 PheValAlaPheSerMetLysAspGluArgGlnGlyGluIleTyrValAlaPheAsnThr 693  
 Db 722 TTGCTTGCCTTCAACCATGAAGGACGAAACCAAGGCGAGATCTAGCTGGCCTTCAACACC 781  
 QY 694 SerHisLeuProAlaValGluLeuProGluTyrAlaGlyArgTyrGluProVal 713  
 Db 782 AGTCACCTTCGGTGTGTTGTTGGCTTCCAGAGCGCTCTGGGTCCGATGGGAGCGGNG 841  
 QY 714 ValAspThrGlyLysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAla 733  
 Db 842 GTGGACACCGGCAAGGAGGACCATATGACTTCTCCTCAGCATGGCCTGCGCATCTGTCT 901  
 QY 734 LeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyr 753  
 Db 902 GTCACCGCTTACCAAGTCTCTCATTTCTCAACTCACTCTATCTCTATGCTCAGCTAC 961  
 QY 754 SerSerValIleLeuValLeuArgProAspVal 764  
 Db 962 TCCTCCATCATCTTGTATTGGCCCTGATGTC 994

RESULT 15  
 US-10-369-493-26296  
 ; Sequence 26296, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 26296  
 ; LENGTH: 2241  
 ; TYPE: DNA  
 ; ORGANISM: Synecocystis sp.  
 US-10-369-493-26296

Alignment Scores:  
 Pred. No.: 7.5e-159 Length: 2241  
 Score: 1389.00 Matches: 305  
 Percent Similarity: 53.86% Conservative: 86  
 Best Local Similarity: 42.01% Mismatches: 251



```

Db      2080 TTGGAATTGCCCCCTCTAAACGATGTTTGATTGGCATCGACTGGTGGATACCTATTTA 2139
Qy      719 ProAlaProTyrAspPhe 724
Db      2140 CCAACTCCGTTGGACTTC 2157

```

Search completed: August 10, 2004, 07:28:27  
Job time : 1509 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 10, 2004, 00:45:10 ; Search time 4809 Seconds  
(without alignments)  
4744.168 Million cell updates/sec

Title: US-09-674-817B-3  
Perfect score: 4212  
Sequence: 1 SPAPRLRRWRNATAGKV.....SNLYPMLSYSSVILVLRPDV 764

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh  
-Q/cgn2\_1/USFT0\_spool/US09674817/runat\_04082004\_165844\_24593/app\_query.fasta\_1.903  
-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -DOOFL=0 -IOOEXT=0  
-UNIT8=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09674817@cgn2\_1.1 3437 @runat\_04082004\_165844\_24593 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hcc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_nam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	1201	28.5	910	13	BQ609719	BQ609719 BRY 5805
2	1117	26.5	737	13	BQ609582	BQ609582 BRY_3559
3	1092	25.9	625	14	CD897205	CD897205 GI174.105C
4	1074	25.9	617	13	BQ997255	BQ997255 H107G18r
5	1053.5	25.0	655	14	CB035933	CB035933 VVA015B02
6	1052	25.0	590	12	BQ267405	BQ267405 BQ267405
7	1038.5	24.7	913	12	BQ444934	BQ444934 GA_Ra002
8	998.5	23.7	753	13	BQ65760	BQ65760 QG5M22.Y
9	986	23.4	578	10	BE493792	BE493792 WHE1275.E
10	981	23.3	637	14	CA781552	CA781552 024A03AF
11	974.5	23.1	697	14	CA199345	CA199345 SCRLFL101
12	948.5	22.5	661	13	BQ039907	BQ039907 PP_L3a000
13	943.5	22.4	622	14	CF041929	CF041929 QGT31h03.
14	943	22.4	536	13	BQ971724	BQ971724 H19H15r
15	904	21.5	519	13	BQ970613	BQ970613 H15C17r
16	894	21.2	508	14	CD890597	CD890597 G118.115A
17	885.5	21.0	591	14	CB605134	CB605134 3529_1.68
18	885	21.0	785	12	BQ591026	BQ591026 BQ591026
19	866.5	20.6	551	14	CB617184	CB617184 3529_1.70
20	863.5	20.5	644	9	AI737641	AI737641 605036B10
21	853.5	20.3	582	13	BU043560	BU043560 PP_L3a001
22	843	20.0	564	12	BQ272361	BQ272361 BQ272361
23	818.5	19.4	759	12	B1176864	B1176864 EST517809
24	816	19.4	729	12	BQ595165	BQ595165 BQ595165
25	814.5	19.3	592	12	B1934640	B1934640 EST554529
26	810.5	19.2	580	12	B1934559	B1934559 EST554448
27	810.5	19.2	712	14	CD442228	CD442228 EL01N0437
28	803.5	19.1	550	13	BU090334	BU090334 8r70803.Y
29	766	18.2	445	13	BU974414	BU974414 HB27N18r
30	764	18.1	438	13	BU971450	BU971450 HB17K14r
31	761.5	18.1	967	14	CK291085	CK291085 EST753799
32	756.5	18.0	558	10	AW832588	AW832588 sm14007.Y
33	753	17.9	438	13	BU971179	BU971179 HB16N12r
34	747	17.7	431	12	BM500514	BM500514 PAC000000
35	745.5	17.7	496	14	CF040681	CF040681 QGT117A05.
36	743.5	17.7	547	12	BM178903	BM178903 saj60H07.
37	738.5	17.5	497	14	CD442761	CD442761 EL01N0417
38	730.5	17.3	473	14	CK101133	CK101133 F023F78.5
39	717.5	17.0	781	14	CD576563	CD576563 UCRPT01.0
40	703.5	16.7	669	14	CD003812	CD003812 VVA015B02
41	703	16.7	469	12	BI075394	BI075394 IP1_20.AC
42	702	16.7	392	13	BU973837	BU973837 HB26B22r
43	696	16.5	584	14	CB877804	CB877804 HP06B23T
44	682.5	16.2	574	9	AI901664	AI901664 618008G03
45	682	16.2	474	14	CD890598	CD890598 G118.115A

ALIGNMENTS

RESULT 1  
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LOCUS BQ609719 BRY 5805 wheat EST endosperm library Triticum aestivum cdna 5',  
DEFINITION mRNA sequence.  
ACCESSION BQ609719  
VERSION BQ609719.1 GI:21559058  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.

```

REFERENCE 1 (bases 1 to 910)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
FEATURES
source
1..910
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
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Pred. No.: 1201.00 Matches: 235
Score: 92.11% Conservative: 10
Percent Similarity: 88.35% Mismatches: 14
Best Local Similarity: 28.51% Indels: 7
Query Match: 13 Gaps: 0
DB:
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DB 786 TATTCGAGGAGGAGCCAAATAGGAGGATGCTTATTCACGCCAAAGATCTCAAGC 727
QY 98 aAspArg-ValThrGluGluValProLeuAspProLeuMetAsnArgThr-GlyAsnVal 117
DB 726 GAATAGGGGTTCACAGGAGGTCCTTGCCTTGAATGAATCGGACCGGGGAAGGTG 667
QY 118 TrpHisValPhe-IleGluGlyGluLeuHisMetLeuTyrGlyTyrArgPheAspGl 137
DB 666 TGGCATGTTTTCATGGAAGGAGGAGCTGCACACATACTTAACGGGAAACAGTTCGACG 607
QY 137 YThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnVal-ValValAspProT 157
DB 606 CGCTTTTTCCTCATCTGGCCCAATACCTTGATGTTCCAAAGTCGGTGGATCCTT 547
QY 157 YAlaLysAlaValIleSerArgGlyGlu-TyrGlyValProAlaArgGlyAsnAsnCys 176
DB 546 ATGCTAAGCAGTGATTAAGCCGAGGAGATATGGTGTTCACGCGCGTGGTAACAATTC 487
QY 177 TrpProGln-MetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAs 196
DB 486 TGGCCTTCAAGATGGCTGGCATATGATCCTCTTCATATAGCACGTTTGATGGAAAGCGA 427
QY 196 pLeuProLeuAspTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPh 216
DB 426 CCTACCTTAAGATATCCTCAAAGGACCTGGTAATATATAGATGCATTCGCTGGGAT 367
QY 216 eThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys 236
DB 366 CAGGAAGCATGATCAAGCAATGTAGACATCCGGGTACTTTTCATTGGAGCTGTGTCCAA 307
QY 236 sLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPh 256
DB 306 GCTTGACTATTTCAGAGAGCTTGGAGTTAATTGTATTGAATTAATGCCCTGCATGAGTT 247
QY 256 eAsnGluLeuGluTyrSerThrSerSerSerLysMetAsnPheThrPheTyrSerThrIl 276
Db 246 CAACGAGCTGGAGTACTCAACCTCTTCTCCAGATGAACCTTTTGGGGATATTTACCAT 187
QY 276 eAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAs 296
Db 186 AAACCTCTTTTTCACCAATGACAGATACATACAGCGGGGATAAAAAACTGTGGCGGTGA 127
QY 296 pAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIl 316
Db 126 TGCATAAATGAGTTCAAAACCTTTTGAAGAGAGGCTCACAACCGGGGAATTGAGTGTAT 67
QY 316 eLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPh 336
Db 66 CCTGAATGTTGCTTCCACCATACAGCTGAGGGAATGAGATGGTCCAGTATTGTCATT 7
QY 336 eLys 337
Db 6 TAAG 3
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LOCUS BRY 5559 wheat EST endosperm library Triticum aestivum cDNA 5',
DEFINITION mRNA sequence.
ACCESSION BQ609582 GI:21558921
VERSION BQ609582.1
SOURCE Triticum aestivum (bread wheat)
KEYWORDS Triticum aestivum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1. (bases 1 to 737)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE Arabidopsis genomic information for interpreting wheat EST
sequences
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
JOURNAL 22478026
MEDLINE 12590341
PUBMED
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
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source
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/cultivar="Wyuna"
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/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
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Pred. No.: 1117.00 Matches: 213
Score: 90.20% Conservative: 8
Percent Similarity: 86.94% Mismatches: 18
Best Local Similarity: 26.52% Indels: 6
Query Match: 13 Gaps: 2
DB:
US-09-674-817B-3 (1-764) x BQ609582 (1-737)
QY 291 LysAsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLys 310
Db 3 AAAAAGCTGTGGCGGTGATGTCATAAATGAGTTCAAAACCTTTTGAAGAGAGGCTCACA 62
QY 311 ArgGlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsn 330

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Db      63  CGGGGAATTCAGGTGATCTCGGATGTTGTTCTTCAACCATACAGCTCAGGGTAATGAGAT 122
Qy      331 GlyProIleLeuSerPheLeuValAspAsnThrTyrTyrMetLeuAlaProLys 350
Db      123  GGTCGAATATATCATTTAGGGGGGTCGATAATACATACATATATATGTTGCACCCAG 182
Qy      351 GlyGluPheTyrAsnTyrSerGlyCysGlyValAsnThrPheAsnCysAsnHisProValVal 370
Db      183  GGAGAGTTTATAAATATTCGCTGGGATACCTTCACTGTAATCATCTCTGTGGTT 242
Qy      371 ArgGlnPheIleValAspCysLeuArgTyrTyrValThrGluMetHisValAspGlyPhe 390
Db      243  CGTCAATTCATTGATGATGTTTAAAGATATCGGTCATGGAATGCAATGCAATGCTGTTT 302
Qy      391 ArgPheAspLeuAlaSerIleMetThrArgGlySerSerLeuTyrAspProValAsnVal 410
Db      303  CGTTTGAATTCATCCATATGACACAGAGTTCCAGTCTGTGGATCCAGTTAACGTG 362
Qy      411 TyrGlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThrProPro 430
Db      363  TATGGAGCTCCCAATAGAGGTGACATGATCACACAGGGACACCTCTTGGTACTCCACCA 422
Qy      431 LeuIleAspMetIleSerAsnAspProIleLeuGlyGlyValIleLeuIleAlaGluAla 450
Db      423  CTTATTCATGATGATGACCAATGACCAATTCITGGAGGGCTCAAGCTCATCTGCTGAAGCA 482
Qy      451 TrpAspAlaGlyGlyLeuTyrGlnValGlyGlnPheProHisTyrAsnValTrpSerGlu 470
Db      483  TGGGATGACAGGAGGCTCTATCAAGTAGTCAATTCCTCACTGGAATGTTGGTCTGAG 542
Qy      471 TrpAsnGlyTyrTrpArgAspIleValArgGlnPheIleLeuGlyThrAsp-GlyPheAl 490
Db      543  TGGAAATGGGAAGTACCGGACATTCGCCCAATTCCTTAAAGGCACTGGTGGGATTTGT 602
Qy      490 aGlyGlyPheAla--GlyCysLeuCysGlySerProHisLeuTyr---GlnAlaGlyGly 508
Db      603  TGGTGGTTTGGCCGAGCTCTTTGTGNAGTCCACACCTATTTCCCGGACGGGGAG 662
Qy      509 ArgLysPro-TrpHisSerIleAsn---PheValCysAlaHisAspGlyPheThrLeuAl 527
Db      663  GGGAAACCTTTGGCCAGTATTCAAAATTTGGTTGTGCCCTGTGATGGATTTACACTGGG 722
Qy      527 aAspLeu 529
Db      723  GGGAAAT 729

CD897205      625 bp      mRNA      linear      EST 14-JUL-2003
G174.105C12F010823 G174 Triticum aestivum cDNA clone G174105C12,
mRNA sequence.
CD897205      1      GI:32671533
CD897205      1      (bases 1 to 625)
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 625)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003);
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr/).
Location/Qualifiers

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Score:          1092.00      Matches:      203
Percent Similarity: 99.02%      Conservative: 0
Best Local Similarity: 99.02%      Mismatches: 2
Query Match:    25.93%      Indels:      2
DB:             14          Gaps:        0

US-09-674-817B-3 (1-764) x CD897205 (1-625)
Qy      544  AsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGlyGluPheAla 563
Db      13   AACAGAGATGGAGAAAATCAATCTTAGCTGGAATTTGTGGGAGGAGGAGATTCGCA 72
Qy      564  ArgLeuSerValIysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMet 583
Db      73   AGATTGCTGTCAAAAGATTGAGGAGAGGACAGATGCGCAATTCCTTTGTTGTCATG 132
Qy      584  ValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGly 603
Db      133  GTTTCTCAAGAGTCCAAATGTTCTACATGGTGATGAATATGCCACACACAAAAGGGGC 192
Qy      604  AsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTrpAspLysLysGlu 623
Db      193  AACACAAATACATACCTGCCATGATCTTAATGTCATTTTTCCTGGGATAAAAAGAA 252
Qy      624  GlnTyrSerGluLeuHisArgPheCysLeuMetThrLysPheArgLysGluCysGlu 643
Db      253  CAATACTCTGAGTTGCCACCGATTCTGTGCTCATGACCAATTCGCAAGGAGTGCGAG 312
Qy      644  GlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGlnPro 663
Db      313  GGCTTGGCTTGGAGACTTTCAAAGCGCCAAACGGCTGAGTGGCATGTCATCAGCCT 372
Qy      664  GlyLysProAspTrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArg 683
Db      373  GGGAGGCTGATTGGTCTGAGATAGCCGATTCGTTGCCCTTTCCATGAAGATGAAGA 432
Qy      684  GlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeuPro 703
Db      433  CAGGGCGAGATCTATGTGGCTTCAACACAGCCACTTACCGGCCCTTGTGTAGCTCCA 492
Qy      704  GluArgAlaGlyArgArgTrpGluProValValAspThrGlyLysProAlaProTyrAsp 723
Db      493  GAGCGCGAGGGCGCGGTGGGAAACCGGTGGTGGACACAGCCAGCCAGCACCATTAGC 552
Qy      724  PheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeu 743
Db      553  TTCTCACCAGCAGCTTACT-GATCGGCTCTCACCATACACAGTTCCTCGCATTC-CTC 610
Qy      744  TyrSerAsnLeuTyr 748
Db      611  TATCCAACTCTTAC 625

RESULT 4
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LOCUS
DEFINITION
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5-PRIME, mRNA sequence.
ACCESSION
BU997255
VERSION
BU997255.1
GI:24274238
KEYWORDS
EST.

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BU997255 617 bp mRNA linear EST 23-OCT-2002  
 HT07G18r HI Hordeum vulgare subsp. vulgare cDNA clone HI07G18

SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 617)  
AUTHORS Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.  
TITLE EST sequencing and analysis in barley (2002)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Stein Nils  
Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert Length: 617 Std Error: 0.00  
Plate: 7 row: G column: 18  
Seq primer: M13rev.

FEATURES  
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ORIGIN  
Alignment Scores:  
Pred. No.: 3,51e-109 Length: 617  
Score: 1074.00 Matches: 192  
Percent Similarity: 97.03% Conservative: 4  
Best Local Similarity: 95.05% Mismatches: 6  
Query Match: 25.50% Indels: 0  
DB: 13 Gaps: 0  
US-09-674-817B-3 (1-764) x BU997255 (1-617)

QY 107 LeuAspProLeuMetAsnArgThrGlyAsnValTrpHisValPheIleGluGlyLeu 126  
DB 11 CTTGACCCCTGATGATCGGACGTGGGACGTGGCATGCTCTTCCTCGTGGCGAGCTG 70  
QY 127 HisAsnMetLeuTyrGlyTyrArgPheAspGlyThrPheAlaProHisCysGlyHisTyr 146  
DB 71 CACGGCATGCTTTATGGGTACAGGTTCCGACGGCACCTTCCTCCTCCTCGGGGACCTAC 130  
QY 147 LeuAspValSerAsnValValAspProTyrAlaLysAlaValIleSerArgGlyGlu 166  
DB 131 TTGATGTTTCCAAATGTTGGTGGATCTCTATGCTTAGCGAGTGTAGACGGGAGGAG 190  
QY 167 TyrGlyValProAlaArgGlyAsnAsnCysTrpProGlnMetAlaGlyMetIleProLeu 186  
DB 191 TATGGTGTTCGGCGCATGGTAACAATTTGGTGGCTCAGATGCTGGCATGATCCCTCT 250  
QY 187 ProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyrProGlnLysAspLeu 206  
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QY 207 ValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSerSerAsnValGluHis 226

Db 311 GTAATATATAGATGCACCTTGGTGGATTCCAGAACATGATTCAAGCAATGTAGACAT 370  
QY 227 ProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLysGluLeuGlyValAsn 246  
Db 371 CCGGGTACTTTCATTTGGGGCTGTGCGAAGCTTGACTATTTCAGAGAGCTTGGAGTTAAT 430  
QY 247 CysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyrSerThrSerSerSer 266  
Db 431 TGTATAGAAATTAATGCCCTGCCATGAGTTCAACGAGCTGGAGTATGCAACCTCTTCTCC 490  
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Db 491 AGATGAACATTTTGGGGATATTCTACCAATAAACTTCTTCCACCAATGACGAGTACAG 550  
QY 287 SerGlyGlyIleLysAsnCysGlyAspAlaIleAsnGluPheLysThrPheValArg 306  
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QY 307 GluAla 308  
Db 611 GAGTCT 616

RESULT 5  
CB035933  
LOCUS  
DEFINITION CB035933 655 bp mRNA linear EST 15-JAN-2003  
VWA015B02.119888 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera cDNA clone VWA015B02.5, mRNA sequence.  
ACCESSION CB035933  
VERSION CB035933.1 GI:27755178  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
REFERENCE 1 (Bases 1 to 655)  
AUTHORS Cramer, G.R. and Cushman, J.C.  
TITLE An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay  
JOURNAL Unpublished (2002)  
COMMENT Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1318  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T3 20mer  
BACKWARD: T7 20mer  
Plate: 015 row: B column: 02  
Seq primer: T3 20mer  
High quality sequence stop: 655.  
Location/Qualifiers  
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ORIGIN  
Alignment Scores: 7.74e-107 Length: 655  
Pred. No.:



Score: 1053.50 Matches: 179  
 Percent Similarity: 90.83% Conservative: 19  
 Best Local Similarity: 82.11% Mismatches: 19  
 Query Match: 25.01% Indels: 1  
 DB: 14 Gaps: 1

US-09-674-817B-3 (1-764) x CB035933 (1-655)

QY 456 LeuTyrGlnValGlyGlnPheProHisTyrAsnValTyrSerGluTyrPheAsnGlyLysTyr 475  
 Db 1 CTTTACCAAGTTGGCATGTTCTCTACTGGGTCCTTGTGTCAGATGGATGGAGATAT 60  
 QY 476 ArgAspIleValArgGlnPheIleLysGlyThrAspGlyPheAlaGlyGlyPheAlaGlu 495  
 Db 61 CGTGACATAGTCGGCAGATTATTAAGGTTTCAGATGGATTCTCGGGCTTTTGTCTGAA 120  
 QY 496 CysLeuCysGlySerProHisLeuTyrGlnAlaGlyGlyValArgLysProThrHisSerIle 515  
 Db 121 TGCCTTTTGGGAGCCCTAATCTGTACAGAGAGGAGGAGAAACCTTGGAAACAGTATC 180  
 QY 516 AsnPheValCysAlaHisAspGlyPheThrLeuAlaAspLeuValTyrTrpAsnLysLys 535  
 Db 181 AACTTTGTGTGGCCACATGATGTTTACGTTGGCTGATTTAGTGACATACACAAAGAG 240  
 QY 536 TyrAsnLeuProAsnGlyGluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsn 555  
 Db 241 CATACAAATGCAATGGAGAGACACAAATGATGGGAGAAATCATATAACACAGCTGGAAC 300  
 QY 556 CysGlyGluGluGlyGluPheAlaArgLeuSerValLysArgLeuArgLysArgGlnMet 575  
 Db 301 TGTGGCAAGAAGGAGATTTCAGATATTTCACTAAGAAATTTAGGAGAAACACAAATG 360  
 QY 576 ArgAsnPhePheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAsp 595  
 Db 361 CGAAATTTCTTTCTTGTGCTCATGTTTCCCAAGGTGTCCTTATGATCTACATGGGTGAT 420  
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 Db 421 GAATATGTCACACAAAGGGGGACACAAATAGTATGGCATGAATATATATGAAC 480  
 QY 616 TyrPheArgTyrAspLysLysGluGln---TyrSerGluLeuHisArgPheCysCysLeu 634  
 Db 481 TACTTCCGATGGGATAAAGAAAGAGTCATTTATCTGATTTCTTCAGATTTTGTGCTT 540  
 QY 635 MetThrLysPheArgLysGlyCysGluGlyLeuGlyLeuGluAspPheProThrAlaLys 654  
 Db 541 ATGTCCAAATCCGCCAAGATGCCAGTCACCTTGAATGACTTCCCAACACGACAG 600  
 QY 655 ArgLeuGlnTrpHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSer 672  
 Db 601 AGGCTGCAGTGGCATGGGGCCACCCTGGGATGCCAGACTGGTCTAAACACAGC 654

## RESULT 6

BJ267405 590 bp mRNA linear EST 09-APR-2002  
 LOCUS  
 DEFINITION  
 aestivum unpublished cDNA library, wh\_oh Triticum  
 accession  
 version  
 keywords  
 source

BJ267405.1 GI:20087755

## ORGANISM

Triticum aestivum (bread wheat)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 590)

## REFERENCE

Ogihara, Y. and Murai, K.  
 Expressed genes in Triticum aestivum  
 Unpublished (2002)  
 Contact: Tadashi Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel.: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.  
 Location/Qualifiers  
 1..590  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="whohlif13"  
 /tissue type="pistil at heading date"  
 /dev stage="Peekes' scale 10.5"  
 /clone\_lib="Y. Ogihara unpublished cDNA library, wh\_oh"

## FEATURES

source

## ORIGIN

Alignment Scores: 9.5e-107 Length: 590  
 Pred. No.: 1052.00 Matches: 187  
 Score: 96.94% Conservative: 3  
 Percent Similarity: 96.94% Mismatches: 6  
 Best Local Similarity: 95.41% Indels: 0  
 Query Match: 24.98% Gaps: 0  
 DB: 12

US-09-674-817B-3 (1-764) x BJ267405 (1-590)

QY 543 AsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrAsnCysGlyGluGlyGluPhe 562  
 Db 3 AACCAACAGNATGGAGAAATACAACTTAGCTGGATTTGTGGGAGGAGGAATTC 62  
 QY 563 AlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeu 582  
 Db 63 GCAAGATTGCTGTCAAAGATTGAGGAGAGGAGATGCCCAATTTCTTTGTTGTC 122  
 QY 583 MetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGly 602  
 Db 123 ATGTTTCTCAGAGATTCCAAATGTTTATATGGCCATGAGTATGCCACCAAGGG 182  
 QY 603 GlyAsnAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLysLys 622  
 Db 183 GGCACCAACAAATACATCTGCCATGATTTCTTATGTCAATTTATTCGCTGGATATAAAA 242  
 QY 623 GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642  
 Db 243 GACAAATCTCTCACTTGCACCGATTTCTGTGCTCATGACCAATTCGCCAAGGATGC 302  
 QY 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTrpHisGlyHisGln 662  
 Db 303 GAGGCTCTTGGCCTTGAGGATTTCCACGCGCCGACCGCTGCAGTGGCATGTGTCATCAG 362  
 QY 663 ProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682  
 Db 363 CCTGGGAAGCCTGATTTGCTGAGAATAGCCGATTCGTTGCCCTTTCCATGAAAGATGAA 422  
 QY 683 ArgGlnGlyGluIleTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702  
 Db 423 AGACAGGGCGAGATCTATGTGGCTTTCAACACGACCACTTACCGCCGTTGTGTAGCTC 482  
 QY 703 ProGluArgAlaGlyArgArgTyrProValValAspThrGlyLysProAlaProTyr 722  
 Db 483 CCGAGCGCACAGGGCGCGGTGGGAACCGGTGGTGGACACAGGCAAGCCAGCACCATAC 542  
 QY 723 AspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGln 738  
 Db 543 GACTTCTCTACTGACGACTTACCTGATCGGCTCTCACCATACACCAG 590

## RESULT 7

BG444934 913 bp mRNA linear EST 15-MAR-2001  
 LOCUS  
 DEFINITION  
 GA\_Ea0026B23f Gossypium arboreum 7-10 dba fiber library Gossypium  
 arboreum cDNA clone GA\_Ea0026B23f, mRNA sequence.  
 accession  
 version  
 keywords

SOURCE  
ORGANISM  
Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 913)  
REFERENCE  
AUTHORS  
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
Henry, D., Wood, I.C., Leslie, A. and Wilkins, T.A.  
TITLE  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATGAGCTCACTATAGGG  
High quality sequence stop: 777.  
FEATURES  
source  
1..913  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="CA\_Ea026B23f"  
/tissue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"  
ORIGIN  
Alignment Scores:  
Pred. No.: 6,65e-105 Length: 913  
Score: 1038.50 Matches: 202  
Percent Similarity: 79.66% Conservative: 33  
Best Local Similarity: 68.47% Mismatches: 51  
Query Match: 24.66% Indels: 11  
DB: 12 Gaps: 4  
US-09-674-817b-3 (1-764) x BG444934 (1-913)  
QY 162 IleserArgGlyGluTyrGlyValProAlaAaGGlyAsnAsnCysTrpProGlnMetAla 181  
Db 26 ATAGCAGAGGGAGGTTGGGGCTTTAGGGCTGAGATAATTTGGGCCCAATGGCC 85  
QY 182 GlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAspLeuProLeuArgTyr 201  
Db 86 GGAATGGTGCCTACTTTCAGATATCATGTTTGGTGGAGGGTATTTACCTTTGAGACAT 145  
QY 202 ProGlnIleAspLeuValIleTyrGluMetHisLeuArgGlyPheThrLysHisAspSer 221  
Db 146 CCACAGAGATCTCATATTTACGAATGCATGCGTGGATATACAAGATGATCACT 205  
QY 222 SerAsnValGluHisProGlyThrPheIleGlyAlaValSerLysLeuAspTyrLeuLys 241  
Db 206 AGTGGGCAAAATTTCTCGACAGTATCTGTTGGTGGAAAGCTTGACCACATTAAG 265  
QY 242 GluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPheAsnGluLeuGluTyr 261  
Db 266 GAACCTTGGAGTCAACTGCATAGATTAATGCCATGTCAGATTCATGAGTTGAGATC 325  
QY 262 SerThrSerSerSer-----LysMetAsnPheTrpGlyTyrSerThrIle 276  
Db 326 TACAGCTACAATCTGTTTTGGGTGACTATATAGTTCAACTTTTGGGCATATCAACAATC 385  
QY 277 AsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGlyArgAsp 296  
Db 386 AATTATTTTCCCCCATGATAGAGGTATTCATCTCTGGTATTCTGTAGCTGTGCTGTAT 445

QY 297 AlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGluValIle 316  
Db 446 GCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 505  
QY 317 LysAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeuSerPhe 336  
Db 506 ATGGATGTTGTTTTCATCAACAGCTGAAGGGCATGAGAAAGGTTCTCAGTTTGTTCATT 565  
QY 337 LysGlyValAsnAsnThrThrTyrMetLeuAlaProLysGlyGluPheTyrAsnTyr 356  
Db 566 AGAGGTGTTGATTAACCTGCTCTATTACATGCTGGCACCTTAAGGAGAGTACTACATTAAT 625  
QY 357 SerGlyCysGlyAsnThrPheAsnAsnHisProValValArgGlnPheIleValAsp 376  
Db 626 TCAGGGTGTGGGAACACATTAACCTGACCATCTCTGCTGCTCAATTTATATATAGAC 685  
QY 377 CysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeuAlaSer 396  
Db 686 TGCTTAAGATATTGGGTAAACAGAAATGATGTCGATGGGTGCGTTGATCTTGTCTTCC 745  
QY 397 IleMetThrArgGlySerSerLeuTrpAspProValAsnValTyrGlyAlaProIleGlu 416  
Db 746 AT-ATGACCAGGAGTAGCGTCTTTGGGATCA-GTAAATGTTATGGGA---GATCTTGAG 800  
QY 417 GlyAspMetIleThrThrGlyThrProLeuValThrProLeuIleAspMetIleSer 436  
Db 801 AAGGGATTGGATACAACTGGC---CCCTCTCAACATCTCCATCGTGGCTGAGTAGT 857  
QY 437 AsnAspProIleLeuGlyValLysLeuIleAlaGluAlaTyr 451  
Db 858 AAG-----ATCTGTACTCGGAGAGGAGCTATATCTGAGCATGG 896  
B0865760 753 bp mRNA linear EST 14-AUG-2002  
QGC5M22.yg.ab1 QG ABCDI lettuce salinas Lactuca sativa cDNA clone  
QGC5M22, mRNA sequence.  
B0865760 GI:22251225  
B0865760.1 GI:22251225  
EST.  
Lactuca sativa  
Lactuca sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.  
1 (bases 1 to 753)  
REFERENCE  
AUTHORS  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
TITLE  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compsgenomics.ucdavis.edu/  
JOURNAL  
COMMENT  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
singleton, see http://cgdb.ucdavis.edu/ for details.  
Plate: QGC5 row: M column: 22.  
FEATURES  
source  
1..753  
/organism="Lactuca sativa"  
/mol\_type="mRNA"  
/cultivar="Salinas"  
/db\_xref="taxon:4236"  
/clone="QGC5M22"  
/lab\_host="E.coli"  
/clone\_lib="QG ABCDI lettuce salinas"  
/note="Vector: pBRCNAsFIAB; The library was constructed

from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at [http://cgdb.ucdavis.edu/TAG\\_SEQ](http://cgdb.ucdavis.edu/TAG_SEQ) Not found"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,45e-100 Length: 753  
 Score: 998.50 Matches: 182  
 Percent Similarity: 80.93% Conservative: 26  
 Best Local Similarity: 70.82% Mismatches: 32  
 Query Match: 23.71% Indels: 17  
 DB: 13 Gaps: 2

US-09-674-817B-3 (1-764) x BQ865760 (1-753)

QY 177 TrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGluGlyAsp 196  
 DB 10 TGGCCG-----CTTGACGGGAGAGAT 33

QY 197 LeuProLeuArgTyrProGlnLysAspLeuValIleTyrGluMetHisLeuArgGlyPhe 216  
 DB 34 CTGCCCTGTCTTCCACAAAGAGATCTGGTGATTTATGAATGATGTTCTCGTGATTT 93

QY 217 ThrLysHisAspSerSerAsnValGluHisProGlyThrPheIleGlyAlaValSerLys 236  
 DB 94 ACAAGGCATGAGTCCAGTAAGACAGAGTCTCTGGTACTTACTTGGTGTAGTGAAAA 153

QY 237 LeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHisGluPhe 256  
 DB 154 CTGTATCATTTAAAGAACTTGGTGTGAATCATAGAGTTTATGCCATGCCATGATTC 213

QY 257 AsnGluLeuGluTyrSerThr-----SerSerSerLysMetAsnPheTrp 271  
 DB 214 ATAGCTGGAGTACTTACGATCAATCTGTCTGGGTGACTACAGTTAAATTTGG 273

QY 272 GlyTyrSerThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLys 291  
 DB 274 GGGTATTCAACTATCAATTAATCTTCCACCTATGTTGAGATATGCTATCTGCTGGTGGT 333

QY 292 AsnCysGlyArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArg 311  
 DB 334 ATGTGGCCTTGATGCAATAAATGAGTTCAAAACAACTTTATTAAGAGCCACACAAACGT 393

QY 312 GlyIleGluValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGly 331  
 DB 394 GGAATCGAGTGCTCATGCTGTTGTTTCAATCACACTGCTGAAGGGAATGAAATGGT 453

QY 332 ProIleLeuSerPheLysGlyValAspAsnThrThrTyrTyrMetLeuAlaProLysGly 351  
 DB 454 CCCATTCTGCTTTTCGAGGTGTTGATACAGTGTCTTTTATATCTTGCACCTAAGGGA 513

QY 352 GluPheTyrAsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArg 371  
 DB 514 GAGTTCTACAACTATTCAGAGTGTGGAACACATTCACCTGCAACCACTTATGTGGCC 573

QY 372 GlnPheIleValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArg 391  
 DB 574 CAATTATAGTAGATCCCTTGAGATATTGGGTAAACAGAGATGCATGTAGATGCAATTCGA 633

QY 392 PheAspLeuAlaSerIleMetThrArgGlySerSerLeuTrpAspProValAsnValTyr 411  
 DB 634 TTGTATCTTGCTCTATCATGACAGAGCCAGCAGTCTTTTGTGATGCGATTAATGTAT 693

QY 412 GlyAlaProIleGluGlyAspMetIleThrThrGlyThrProLeuValThr 428  
 DB 694 CGAATCAAGTAGAAGATGATTACTGACACCGGGTCTCATCTCTCATCACC 744

## RESULT 9

BE493792

## LOCUS

## DEFINITION

BE493792

## ACCESSION

BE493792

## VERSION

BE493792.1

## KEYWORDS

EST.

## SOURCE

Secale cereale

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Secale.

## REFERENCE

1 (bases 1 to 578)

## AUTHORS

Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.

## TITLE

The structure and function of the expressed portion of the wheat genomes - Another cDNA library from rye

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

## FEATURES

Location/Qualifiers

1..578

/organism="Secale cereale"

/mol\_type="mRNA"

/cultivar="Blanco"

/db\_xref="taxon:4550"

/clone="WHE1275.E05.I09"

/tissue\_type="Anther"

/dev\_stage="Adult plant before anthesis"

/lab\_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

## ORIGIN

Alignment Scores:

Pred. No.: 2.29e-99 Length: 578

Score: 986.00 Matches: 179

Percent Similarity: 96.34% Conservative: 5

Best Local Similarity: 93.72% Mismatches: 7

Query Match: 23.41% Indels: 1

DB: 10 Gaps: 0

US-09-674-817B-3 (1-764) x BE493792 (1-578)

## QY

543 AsnAsnArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGlyGluPhe 562

## DB

6 GACAACAGAGATGAGAAAAATAC-AATCTTAGCTGGAACGTGCGGAGGAGAGATTC 64

## QY

563 AlaArgLeuSerValLysArgLeuArgLysArgGlnMetArgAsnPheValCysLeu 582

## DB

65 GCAGATGTCAGTCACAAAGATTCAGAGAGGAGGAGATGCGCAATTCCTTGTGTC 124

QY 583 MetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrIysGly 602  
 Db 125 ATGGTTTCTCAAGGAGTTCCAAATGTTTACATGGCGCATGAATATGGCCACACAAAAGG 184  
 QY 603 GlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTTPAspIys 622  
 Db 185 GGCACAAACAAATACATACATGCTATGATTTCTTAATGCAATATTTTCGTGGATTAATAA 244  
 QY 623 GluGlnTyrSerGlnLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys 642  
 Db 245 GAACAATACCTGACTGTGACGATTCCTGCTGCTCATGCCAAATTCGGCAAGGAGTGC 304  
 QY 643 GluGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGlnTTPHisGlyHisGln 662  
 Db 305 GAGGGTCTTGGGCTTGGAGACTTTCCAAACGGCTGAACGGTTCAGTGGCATGGTCATCAG 364  
 QY 663 ProGlyLysProAspTTPSerGluAsnSerArgPheValAlaPheSerMetLysAspGlu 682  
 Db 365 CTGGGAAGCCTGATGCTGCTGAGAAAGCCGATTCGTTGCTTTCCATGAAGATGAA 424  
 QY 683 ArgGlnGlyGluLeuTyrValAlaPheAsnThrSerHisLeuProAlaValValGluLeu 702  
 Db 425 ACAAAAGAGTGAGATCTATGCTGCTTCAACACCGCCACTTACCGGCGGCTTGTGAATC 484  
 QY 703 ProGluArgAlaGlyArgArgTTPGluProValValAspThrGlyLysProAlaProTyr 722  
 Db 485 CCAGAGCGCACAGGCGACCGGTGGNACCGGTGGTGGACACAGGAAGGAGACCATAT 544  
 QY 723 AspPheLeuThrAspAspLeuProAspArgAla 733  
 Db 545 GACTTCTCACCACGACTTACCTGATCGCGT 577

## RESULT 10

CA781552 637 bp mRNA linear EST 03-DEC-2002  
 LOCUS 024A03AF Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA  
 DEFINITION sequence.

ACCESSION CA781552

VERSION CA781552.1 GI:26019585

KEYWORDS Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1 (bases 1 to 637)  
 Lundgaard,M., Emmeren,J., Nielsen,K.L., Wilson,I., Somerville,S.  
 and Wellinder,K.G.  
 EST sequencing of Erysiphe cichoracearum infected Arabidopsis  
 plants

## TITLE

Unpublished (2002)

## JOURNAL

Contact: Karen G. Wellinder

Institut for bioteknologi

Aalborg Universitet

Sohngaardsholmsvej 49, 9000 Aalborg, Denmark

Tel: +45 96358467

Fax: +45 98141808

Email: kgw@bio.au.dk.

## FEATURES

source

1 637

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/strain="Columbia"

/db\_xref="taxon:3702"

/dev\_stage="Plant 3 weeks old, three days post infection"

/clone\_lib="Infected Arabidopsis Leaf"

/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA

library of Arabidopsis and E. cichoracearum infected leaf

from three weeks old Arabidopsis plants. Plants were

harvested 3 days after infection and mRNA oligo dt

selected."

## ORIGIN

## Alignment Scores:

Pred. No.: 9,88e-99 Length: 637  
 Score: 981.00 Matches: 172  
 Percent Similarity: 89.05% Conservative: 15  
 Best Local Similarity: 81.90% Mismatches: 20  
 Query Match: 23.29% Indels: 3  
 DB: 14 Gaps: 2

US-09-674-817B-3 (1-764) x CA781552 (1-637)

QY 445 LysLeuIleAlaGluAlaTrpAspAlaGlyGlyLeuTyrGlnValGlnPheProHis 464  
 Db 12 AACCTAATAGCTGAAGCATGGGATGGGCTGTACCAAGTTGGCATGTTTCCACAC 71  
 QY 465 TrpAsnValTrpSerGluTrpAsnGlyLysTyrArgAspIleValArgGlnPheIleLys 484  
 Db 72 TGGGGTATTGGTCTCAGTGGAAATGGAAAGTTTGGGATGTTGTGAGACAGTTTCAATAA 131  
 QY 485 GlyThrAspGlyPheAlaGlyGlyPheAlaGluCysLeuCysGlySerProHisLeuTyr 504  
 Db 132 GGACCGATGGCTTTTCTGGTGTCTTGTGAATGCTCTGTGGAAGCCCAATCTGTAC 191  
 QY 505 GlnAlaGlyGlyArgLysProTrpHisSerIleAsnPheValCysAlaHisaspGlyPhe 524  
 Db 192 CAG---GGAGGTAGGAACCTTGGCACAGCATCAATTTTATATGTGCGCATGATGTTT 248  
 QY 525 ThrLeuAlaAspLeuValThrTyrAsnLysLysTyrAsnLeuProAsnGlyGluAsnAsn 544  
 Db 249 ACGTTGGCAGATTAGTACTTACACAAATAGATAAATCTTGGCAATGGAGAGAGAT 308  
 QY 545 ArgAspGlyGluAsnHisAsnLeuSerTrpAsnCysGlyGluGluGluPheAlaArg 564  
 Db 309 AATGATGGAGAGAATCACAAATTACAGCTGGAACCTGTGGAGAGGAGGAGACTTTGCGAGT 368  
 QY 565 LeuSerValLysArgLeuArgLysArgGlnMetArgAsnPhePheValCysLeuMetVal 584  
 Db 369 ATCTCGGTGAAGAGACTTAAGAAACACAGATCGGAATTTCTTTGTTCCCTCATGGTT 428  
 QY 585 SerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyLysAsn 604  
 Db 429 TCCCAAGGTGTCCTCAATGATTTACATGGGAGATGAATATGGCCATATAAAGGGGAAAC 488  
 QY 605 AsnAsnThrTyrCysHisaspSerTyrValAsnTyrPheArgTrpAspLysGluGln 624  
 Db 489 AACACACGATTGTCCTACACTATATGAACATTTTTCGGTGGGATACACAGGAAGA 548  
 QY 625 ---TyrSerGluLeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCys-Gl 643  
 Db 549 GCATTTCTGACTTCTCAGATTCTGCCGTATTTCTTATCAAGTTTCGTGATGAATCTTGA 608  
 QY 643 uGlyLeuGlyLeuGluAspPheProThr 652  
 Db 609 ATCACTTGGCTTGAATGATTCCCAACA 636

## RESULT 11

CA199345

LOCUS SCLFL1011G11.9 FL1 Saccharum officinarum cDNA clone SCLFL1011G11

DEFINITION 5', mRNA sequence.

ACCESSION CA199345

VERSION CA199345.1 GI:35231514

KEYWORDS EST

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

REFERENCE 1 (bases 1 to 697)

AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

TITLE The libraries that made SUCEST

JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

COMMENT Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

CA199345 697 bp mRNA linear EST 25-SEP-2003  
 LOCUS SCLFL1011G11.9 FL1 Saccharum officinarum cDNA clone SCLFL1011G11  
 DEFINITION 5', mRNA sequence.

ACCESSION CA199345

VERSION CA199345.1 GI:35231514

KEYWORDS EST

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

REFERENCE 1 (bases 1 to 697)

AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

TITLE The libraries that made SUCEST

JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

COMMENT Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parrada@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bccc.br/facv.unesp.br  
Plate: 011 row: G column: 11  
Seq primer: T7 promoter primer.  
Location/Qualifiers

# FEATURES

1. .697  
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/clone="SCRLFL1011G11"  
/lab\_host="DH10B"  
/clone\_lib="FL1"  
/note="Organ: Inflorescence at beginning of development  
(1cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI;  
An unidirectional cDNA library generated from  
[inflorescence at beginning of development (1cm-long)].  
cDNA was prepared from polyA+ mRNA using Superscript  
Plasmid System Kit (Invitrogen). The double-strand cDNAs  
were fractionated in a sepharose CL-2B 40cm-columns and  
fragments sizing between 0.8 and 1.5 Kb were  
directionally cloned into the vector. Details  
source of RNA and library construction can be obtained at  
http://sucest.lad.ic.unicamp.br/public"

## ORIGIN

Alignment Scores:  
Pred. No.: 6.19e-98 Length: 697  
Score: 974.50 Matches: 179  
Percent Similarity: 91.79% Conservative: 11  
Best Local Similarity: 86.47% Mismatches: 16  
Query Match: 23.14% Indels: 1  
DB: 14 Gaps: 1

US-09-674-817B-3 (1-764) x CA199345 (1-697)

QY 559 GluGlyGluPheAlaArgLeuSerValLysArgLeuGlyArgGlnMetArgAsnPhe 578  
Db 1 GAAGGAGATTTCGAGTTTGTTCAGTCCGAAATTAAGGAAGAGCAATGGCAATTTT 60  
QY 579 PheValCysLeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGly 598  
Db 61 TTTGTTGTCTCATGTTTCTCAGGAGTTCCAAATGTTCTACATGGCGCATGAATGTT 120  
QY 599 HisThrLysGlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArg 618  
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QY 619 TrpAspLysLys---GluGlnTyrSerGluLeuHisArgPheCysCysLeuMetThrLys 637  
Db 181 TGGGATAAGAGGAAGAAACAATCTCTGATTGTGTACAGATTCTGTGCTCATGACCAA 240  
QY 638 PheArgLysGlyCysGlyLeuGlyLeuGluAspPheProThrAlaLysArgLeuGln 657  
Db 241 TTCGGAAGGAATGTGAATCTCTTGGTCTGTGAGGACTTCCGACTTCAGAACGGTTGCAA 300  
QY 658 TrpHisGlyHisGlnProGlyLysProAspTyrSerGluAsnSerArgPheValAlaPhe 677  
Db 301 TGGCAGGTCATCAGCTGGGAGGCTGACTGTGTGGAGGAGCGGATTCGTTCCCTTC 360  
QY 678 SerMetLysAspGluArgGlnGlyLeuTyrValAlaPheAsnThrSerHisLeuPro 697  
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QY 698 AlaValValGluLeuProGluArgAlaGlyArgTyrGluProValValAspThrGly 717  
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QY 718 LysProAlaProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHis 737  
Db 481 AAAGAAGCACCTATGACTTCTCACCAGTGGTTTACAGACCGTGTGTCCACCGTTTAC 540  
QY 738 GlnPheSerHisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIle 757  
Db 541 CAGTTCCTTTCATTTCTCACTCCAACTCTACCTATGCTTAGCTACTCTTCTTATATC 600  
QY 758 LeuValLeuArgProAspVal 764  
Db 601 CCTGTATTGGCCCTGATTT 621

## RESULT 12

BU039907

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Abbott, A.

Dept of Genetics and Biochemistry

Clemson University

122 Long Hall, Clemson University, Clemson, SC 29634, USA

Tel: 864 656 3060

Fax: 864 656 6879

Email: aalbert@clemson.edu

Total High Quality bases = 537

Seq primer: TAATACGACTCACTATAGG

High quality sequence stop: 661.

Location/Qualifiers

1. .661

/organism="Prunus persica"

/mol\_type="mRNA"

/cultivar="Loring"

/db\_xref="taxon:3760"

/clone="PP LeA0004E05f"

/tissue\_type="Mesocarp"

/lab\_host="E. coli"

/clone\_lib="Peach developing fruit mesocarp"

/note="Vector: pBluescript II SK(-); Site 1: EcoRI;

Site 2: XhoI; authority=Prunus persica L. Batsh; The

sequence has been trimmed to remove vector sequence and

contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis go to

http://www.genome.clemson.edu/projects/peach. To order

this clone go to http://www.genome.clemson.edu/orders"

## ORIGIN

Alignment Scores:

Pred. No.: 4.64e-95 Length: 661

Score: 948.50 Matches: 163

Percent Similarity: 87.16% Conservative: 27

Best Local Similarity: 74.77% Mismatches: 27

Query Match: 22.52% Indels: 1

DB: 13 Gaps: 1

US-09-674-817B-3 (1-764) x BU039907 (1-661)

QY 542 GluAsnAsnArgAspGlyGluAsnHisAsnLeuSerTyrAsnCysGlyGluGlyGlu 561

Db 3 GAACACCAATGATGAGAGAGTCAATAATAGTGGAACTGTGGACAGGAGGAGAG 62

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 QY 582 LeuMetValSerGlnGlyValProMetPheTyrMetGlyAspGluTyrGlyHisThrLys 601  
 Db 123 CTCATGTTTCCCAAGGTTCCTCATATATATATATATATATATATATATATATAT 182  
 QY 602 GlyGlyAsnAsnThrTyrCysHisAspSerTyrValAsnTyrPheArgTyrAspLys 621  
 Db 183 GGAGGAAACAAACACATATTCGATGATATATATATATATATATATATATATATAT 242  
 QY 622 LysGluGlnTyrSer---GluLeuHisArgPheCysCysLeuMetThrLysPheArgLys 640  
 Db 243 AAGGAAAGATCTCATGAGCTTTTTCAGATTTTCTGCTTATGACCAATTCGCGAC 302  
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 Db 303 GAATCGGAGTCACTGGGCTTAAATGACTTCCCAACAGCAGAGAGGCTGCAGTGGCATGGT 362  
 QY 661 HisGlnProGlyLysProAspTyrPheGluAsnSerArgPheValAlaPheSerMetLys 680  
 Db 363 CATGCTCCCTGGGCTACCACTGGTCTGAAACAAGCGCTTTGTGCTTTTACTCTGATG 422  
 QY 681 AspGluArgGlnGlyGluLeuTyrValAlaPheAsnThrSerHisLeuProAlaValVal 700  
 Db 423 GACTCAGTGAAGAGAGAGCTGATATATGCTTCAATGCCAGGCATTTACCGCAACCAT 482  
 QY 701 GluLeuProGluArgAlaGlyArgTyrGluProValValAspThrGlyLysProAla 720  
 Db 483 ACACCTCCAGAGAGGCTGGATACAGATGGGATCCCTGGTAGACACAGCAGAGCTGCT 542  
 QY 721 ProTyrAspPheLeuThrAspAspLeuProAspArgAlaLeuThrIleHisGlnPheSer 740  
 Db 543 CCAATTGACTTCTTCTAGTACCTCCAGCAAGAGATATGCGATTAAACAGTACCTG 602  
 QY 741 HisPheLeuTyrSerAsnLeuTyrProMetLeuSerTyrSerSerValIleLeu 758  
 Db 603 CACTTTCTTGATGCCAATTATATCTATCTGCTAAGTATTCTTCAATCATCTCTA 656  
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 CF041929  
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 ACCESSION  
 VERSION  
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 SOURCE  
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 622)  
 Genoplatne.  
 Genoplatne, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplatne  
 Genoplatne  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>)  
 and <http://genoplatne-info.infobiogen.fr/>.  
 Location/Qualifiers  
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 FEATURES  
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ORIGIN  
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 Pred. No.: 943.50 Matches: 171  
 Score: 93.40% Conservative: 13  
 Percent Similarity: 86.80% Mismatches: 12  
 Best Local Similarity: 22.40% Indels: 1  
 Query Match: 14 Gaps: 1  
 DB:  
 US-09-674-817b-3 (1-764) x CF041929 (1-622)  
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 Db 4 CCGGTAAGGAAGAGGCAAAATGCGCAATTTCTTTGTTGTTCTATGTTCTCAGGGAGTT 63  
 QY 589 ProMetPheTyrMetGlyAspGluTyrGlyHisThrLysGlyGlyAsnAsnThrTyr 608  
 Db 64 CCAATGTTTACATGGCGCATGAATATGTTCAACAAGGAGGAGGAAACAACATACGTAC 123  
 QY 609 CysHisAspSerTyrValAsnTyrPheArgTyrAspLysLys---GluGlnTyrSerGlu 627  
 Db 124 TGCATGACCATATATGTCACATATTTCCGTGGATTAAGAAGGAACAACAATCTCTGAT 183  
 QY 628 LeuHisArgPheCysCysLeuMetThrLysPheArgLysGluCysGluGlyLeuGlyLeu 647  
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 QY 648 GluAspPheProThrAlaLysArgLeuGlnTyrHisGlyHisGlnProGlyLysProAsp 667  
 Db 244 GAGACTTCCCGACTTCAGAACGTTGAATGGCAGGTTCATCAGCCCGGAAGCCTGAC 303  
 QY 668 TrpSerGluAsnSerArgPheValAlaPheSerMetLysAspGluArgGlnGlyGluLeu 687  
 Db 304 TGGTCAGAGCAAGCGATTCGTTGCTTCCCATCAGAGGACGAAACCAAGGCGAGATC 363  
 QY 688 TyrValAlaPheAsnThrSerHisLeuProAlaValIleGluLeuProGluArgAlaGly 707  
 Db 364 TAGGTGGCTTCAACACCATGCTTCCGTGGTGTGTCGGCTTCCAGAGGCTCTGGG 423  
 QY 708 ArgArgTyrGluProValValAspThrGlyLysProAlaPheTyrAspPheLeuThrAsp 727  
 Db 424 TTCCGATGGAGCGGTGGTGGACACCGGCAAGAGGACCATATGATTCCTCACCAGAT 483  
 QY 728 AspLeuProAspArgAlaLeuThrIleHisGlnPheSerHisPheLeuTyrSerAsnLeu 747  
 Db 484 GGCTACACAGATCGTGTGCTCACCCTTCCAGCTTCTCTCAATTTCTCAATCTCAATCTC 543  
 QY 748 TyrProMetLeuSerTyrSerSerValIleLeuValLeuArgProAspVal 764  
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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
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 SOURCE  
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 Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 1 (bases 1 to 536)  
 Raddchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.  
 Barley ESTs from developing seeds  
 Unpublished (2002)  
 Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 BU971724 536 bp mRNA linear EST 22-OCT-2002  
 HB19H15r BC Hordeum vulgare subsp. vulgare cDNA clone HB19H15  
 S-PRIME, mRNA sequence.  
 BU971724  
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 Hordeum vulgare subsp. vulgare  
 Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 1 (bases 1 to 536)  
 Raddchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.  
 Barley ESTs from developing seeds  
 Unpublished (2002)  
 Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany

Tel: 039482-5522  
 Fax: 039482-5595  
 Email: stein@pk-gatersleben.de  
 Insert Length: 536 Std Error: 0.00  
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 Location/Qualifiers  
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ORIGIN

Alignment Scores:  
 Pred. No.: 1,33e-94 Length: 536  
 Score: 943.00 Matches: 169  
 Percent Similarity: 97.71% Conservative: 2  
 Best Local Similarity: 96.57% Mismatches: 4  
 Query Match: 22.39% Indels: 0  
 DB: 13 Gaps: 0

US-09-674-817B-3 (1-764) x BU971724 (1-536)

QY 135 PheAspGlyThrPheAlaProHisCysGlyHisTyrLeuAspValSerAsnValVal 154  
 Db 12 TTCAGCGGACCTTCCTCTCTCTACTCGGGGGACTACTTGTGATTTCAATGTTGGTG 71  
 QY 155 AspProTyrAlaLysAlaValIleSerArgGlyGluTyrGlyValProAlaArgGlyAsn 174  
 Db 72 GATCCTTATGCTAAGGACGATGATAGCGGGAGGAGTATGTTGTCGGCGCATGTTAAC 131  
 QY 175 AsnCysTrpProGlnMetAlaGlyMetIleProLeuProTyrSerThrPheAspTrpGlu 194  
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 Db 192 GCGGACCTACCTTAAGATATCTCAAAGGACCTGTGATATATAGACATGCTTGGT 251  
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 QY 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254  
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 QY 255 GluPheAsnGluLeuGluTyrSerThrSerSerLysMetAsnPheTrpGlyTyrSer 274  
 Db 372 GAGTTCAACGAGCTGGAGTATGCAACCTCTCTTCCAAAGATGAACCTTTTGGGGATATCT 431  
 QY 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294  
 Db 432 ACCATTAATCTCTTTTCAACATGACGAGATACAGTACGTACGTGGGATATAAATCTGGG 491  
 QY 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHis 309

Db 492 CGTGATGGCAATAACGAGTTCAAACTTTTGTAGAGAGTCTCAC 536  
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 5-PRIME, mRNA sequence.  
 BU970613  
 BU970613.1 GI:24221406  
 EST.  
 SOURCE  
 ORGANISM  
 Hordeum vulgare subsp. vulgare  
 Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Scrophophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 1 (bases 1 to 519)  
 Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.  
 Barley ESTs from developing seeds  
 Unpublished (2002)  
 Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 Tel: 039482-5522  
 Fax: 039482-5595  
 Email: stein@pk-gatersleben.de  
 Insert Length: 519 Std Error: 0.00  
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 /lab\_host="XL10-Gold"  
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 /notes="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP(days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Alignment Scores:  
 Pred. No.: 2,95e-90 Length: 519  
 Score: 904.00 Matches: 163  
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 Best Local Similarity: 96.45% Mismatches: 2  
 Query Match: 21.46% Indels: 0  
 DB: 13 Gaps: 0

US-09-674-817B-3 (1-764) x BU970613 (1-519)

QY 235 SerLysLeuAspTyrLeuLysGluLeuGlyValAsnCysIleGluLeuMetProCysHis 254  
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 QY 255 GluPheAsnGluLeuGluTyrSerThrSerSerLysMetAsnPheTrpGlyTyrSer 274  
 Db 72 GAGTTCAACGAGCTGGAGTATGCAACCTCTCTTCCAAAGATGAACCTTTTGGGGATATCT 131  
 QY 275 ThrIleAsnPhePheSerProMetThrArgTyrThrSerGlyGlyIleLysAsnCysGly 294  
 Db 432 ACCATTAATCTCTTTTCAACATGACGAGATACAGTACGTACGTGGGATATAAATCTGGG 491  
 QY 295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHis 309



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Db      132 ACCATAAAGCTTTTCCACCAATGACGAGATACAGTCAGGTGGGATATAAAAACTGTGGG 191
QY      295 ArgAspAlaIleAsnGluPheLysThrPheValArgGluAlaHisLysArgGlyIleGlu 314
Db      192 CGTGATGGGATATAAACGAGTTCAAAACTTTTGTAAAGAGAGTCTCACAAAACGGGGAAATTGAG 251
QY      315 ValIleLeuAspValValPheAsnHisThrAlaGluGlyAsnGluAsnGlyProIleLeu 334
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QY      335 SerPheLysGlyValAspAsnThrThrTyrrMetLeuAlaProLysGlyGluPheTyr 354
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QY      355 AsnTyrSerGlyCysGlyAsnThrPheAsnCysAsnHisProValValArgGlnPheIle 374
Db      372 AACTATCTGGCTGTGGGAATACCTTCAACTGTAAATCATCTCTGGGTTCGTCATTTTATT 431
QY      375 ValAspCysLeuArgTyrTrpValThrGluMetHisValAspGlyPheArgPheAspLeu 394
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QY      395 AlaSerIleMetThrArgGlySerSer 403
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